

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 08:43:19 ; Search time 1609 Seconds
(without alignments)
3534.144 Million cell updates/sec

Title: US-09-925-139-3_COPY_1631_1769

Perfect score: 139

Sequence: 1 ggaatggggcttagcagaa.....ctatcctaaggccactgg 139

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.em.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rtd.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sv.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	21	15.1	21	6	BD102270	BD102270 Method of
C 2	17.6	12.7	30	11	BX323474	BX323474 Arabidops
C 3	17.2	12.4	22	6	E25734	E25734 Method for
C 4	16.8	12.1	21	6	BD101979	BD101979 Novel G P
C 5	16.8	12.1	21	6	BD131270	BD131270 Novel G P
C 6	16.8	12.1	30	6	AR262363	AR262363 Sequence
C 7	16.2	11.7	22	6	AR129513	AR129513 Sequence
C 8	16.2	11.7	28	6	E24992	E24992 Apoptosis-i
C 9	16.2	11.7	29	6	AX597968	AX597968 Sequence
C 10	16.2	11.7	30	6	AR018179	AR018179 Sequence
C 11	16.2	11.7	30	6	AX180867	AX180867 Sequence
C 12	16	11.5	25	6	E28689	E28689 Primer for
C 13	16	11.2	26	6	A64642	A64642 Sequence 8
C 14	15.6	11.2	30	6	AR009754	AR009754 Sequence
C 15	15.6	11.2	30	6	I73485	I73485 Sequence 7
C 16	15.6	11.2	30	6	I81194	I81194 Sequence 7
C 17	15.4	11.1	25	6	AX081599	AX081599 Sequence
C 18	15.4	11.1	25	6	AX374780	AX374780 Sequence
C 19	15.4	11.1	29	6	BD169474	BD169474 Novel gua
C 20	15.2	10.9	20	6	AX323427	AX323427 Sequence
C 21	15.2	10.9	23	6	AR142933	AR142933 Sequence
C 22	15.2	10.9	30	6	AR277835	AR277835 Sequence
C 23	15.2	10.9	30	6	AR279994	AR279994 Sequence
C 24	15.2	10.9	30	6	BD128452	BD128452 Solid pha
C 25	15.2	10.9	30	6	BD133164	BD133164 Method of
C 26	15.2	10.9	30	6	I08474	I08474 Sequence 12
C 27	15	10.8	25	6	AR147819	AR147819 Sequence
C 28	15	10.8	25	6	AX534165	AX534165 Sequence
C 29	15	10.8	25	6	AX534166	AX534166 Sequence
C 30	15	10.8	25	6	AX534167	AX534167 Sequence
C 31	15	10.8	26	6	A62920	A62920 Sequence 16
C 32	15	10.8	26	6	I09030	I09030 Sequence 1
C 33	15	10.8	29	6	AR174575	AR174575 Sequence
C 34	15	10.8	29	6	AX280176	AX280176 Sequence
C 35	15	10.8	29	6	AX598144	AX598144 Sequence
C 36	15	10.8	30	6	I26957	I26957 Sequence 6
C 37	14.8	10.6	25	6	AX196921	AX196921 Sequence
C 38	14.8	10.6	27	6	BD133891	BD133891 Alkali ce
C 39	14.8	10.6	30	6	AX078481	AX078481 Sequence
C 40	14.8	10.6	30	6	E07789	E07789 PCR primer
C 41	14.6	10.5	24	6	AX172298	AX172298 Sequence
C 42	14.6	10.5	24	6	AX291985	AX291985 Sequence
C 43	14.6	10.5	24	6	AX300811	AX300811 Sequence
C 44	14.6	10.5	25	6	AX534168	AX534168 Sequence
C 45	14.6	10.5	25	6	AX534169	AX534169 Sequence
C 46	14.6	10.5	29	6	AR019082	AR019082 Sequence
C 47	14.6	10.5	30	6	AR135100	AR135100 Sequence
C 48	14.6	10.5	30	6	AX015112	AX015112 Sequence
C 49	14.6	10.5	30	6	AX611235	AX611235 Sequence
C 50	14.6	10.5	30	6	AX611566	AX611566 Sequence
C 51	14.4	10.4	20	6	AX293741	AX293741 Sequence
C 52	14.4	10.4	20	6	AX488425	AX488425 Sequence
C 53	14.4	10.4	20	6	BD171443	BD171443 Nucleic a
C 54	14.4	10.4	24	6	AX112094	AX112094 Sequence
C 55	14.4	10.4	24	6	AX289108	AX289108 Sequence
C 56	14.4	10.4	24	6	AX44387	AX44387 Sequence
C 57	14.4	10.4	25	6	AX430741	AX430741 Sequence
C 58	14.4	10.4	25	6	AX697107	AX697107 Sequence
C 59	14.4	10.4	26	6	AR061819	AR061819 Sequence
C 60	14.4	10.4	26	6	AR090522	AR090522 Sequence
C 61	14.4	10.4	26	6	AR090530	AR090530 Sequence
C 62	14.4	10.4	26	6	AR197557	AR197557 Sequence
C 63	14.4	10.4	26	6	AR197565	AR197565 Sequence
C 64	14.4	10.4	26	6	AR252810	AR252810 Sequence
C 65	14.4	10.4	26	6	AR259711	AR259711 Sequence

66 14.4 10.4 26 6 AR259719 Sequence
67 14.4 10.4 26 6 BD014707
68 14.4 10.4 27 6 A32001
69 14.4 10.4 27 6 AR109658 Sequence
70 14.4 10.4 27 6 AR109660 Sequence
71 14.4 10.4 27 6 AR175481
72 14.4 10.4 27 6 AR537208 Sequence
73 14.4 10.4 28 6 AX105646
74 14.4 10.4 28 6 AX108637 Sequence
75 14.4 10.4 28 6 AX268878
76 14.4 10.4 28 6 BD102107
77 14.4 10.4 28 6 E48769
78 14.4 10.4 29 6 AX588102 Sequence
79 14.4 10.4 29 6 AX642889
80 14.4 10.4 30 6 A39952
81 14.4 10.4 30 6 AR000087
82 14.4 10.4 30 6 AR016710
83 14.4 10.4 30 6 AR016711
84 14.4 10.4 30 6 AR054423
85 14.4 10.4 30 6 AR064910
86 14.4 10.4 30 6 AR109710
87 14.4 10.4 30 6 AR243697
88 14.4 10.4 30 6 I50069
89 14.4 10.4 30 6 I50070
90 14.4 10.4 30 6 I50106
91 14.4 10.4 30 6 I50107
92 14.2 10.2 20 6 AR011791
93 14.2 10.2 20 6 AR025499
94 14.2 10.2 20 6 AR211960
95 14.2 10.2 20 6 AR281496
96 14.2 10.2 20 6 E08471
97 14.2 10.2 20 6 I26707
98 14.2 10.2 25 6 AR028129
99 14.2 10.2 25 6 AR030305
100 14.2 10.2 25 6 I42124
101 14.2 10.2 27 6 AR116914
102 14.2 10.2 27 6 AR152252
103 14.2 10.2 27 6 AR154789
104 14.2 10.2 27 6 AR182531
105 14.2 10.2 27 6 AR113849
106 14.2 10.2 27 6 AX116588
107 14.2 10.2 27 6 AX117036
108 14.2 10.2 27 6 AX304425
109 14.2 10.2 27 6 AX451838
110 14.2 10.2 27 6 BD074012
111 14.2 10.2 28 6 AR265212
112 14.2 10.2 28 6 AX339688
113 14.2 10.2 28 6 AX351768
114 14.2 10.2 28 6 AX458824
115 14.2 10.2 29 6 AR012146
116 14.2 10.2 29 6 AR091248
117 14.2 10.2 29 6 AR198283
118 14.2 10.2 29 6 AR260437
119 14.2 10.2 30 6 AR024460
120 14.2 10.2 30 6 AR176004
121 14.2 10.2 30 6 AR308620
122 14.2 10.2 30 6 AR308639
123 14.2 10.2 30 6 AR306692
124 14.2 10.2 30 6 AX009400
125 14.2 10.2 30 6 AX155549
126 14.2 10.2 30 6 AX472252
127 14.2 10.2 30 6 AX611465
128 14.2 10.2 30 6 AX611467
129 14.2 10.2 30 6 AX611469
130 14.2 10.2 30 6 AX611470
131 14.2 10.2 30 6 AX694371
132 14.2 10.2 30 6 I63333
133 14 10.1 20 6 A06347
134 14 10.1 22 6 A94117
135 14 10.1 22 6 AR232639
136 14 10.1 22 6 AX011202
137 14 10.1 23 6 AX327669
138 14 10.1 23 6 AX452265

AR259719 Sequence
BD014707 Cyclic nu
A32001 primer (S22)
AR109658 Sequence
AR109660 Sequence
AX175481
AX537208 Sequence
AX105646
AX108637 Sequence
AX268878
BD102107 A novel a
E48769 Novel polyp
AX588102 Sequence
AX642889 Sequence
A39952 Sequence 9
AR000087
AR016710 Sequence
AR016711 Sequence
AR054423 Sequence
AR064910 Sequence
AR109710 Sequence
AR243697 Sequence
I50069 Sequence 2
I50070 Sequence 3
I50106 Sequence 2
I50107 Sequence 3
AR011791 Sequence
AR025499 Sequence
AR211960 Sequence
AR281496 Sequence
E08471 Primer. 9/1
I26707 Sequence 2
AR028129 Sequence
AR030305 Sequence
I42124 Sequence 19
AR116914 Sequence
AR152252 Sequence
AR154789 Sequence
AR182531 Sequence
AX113849 Sequence
AX116588 Sequence
AX117036 Sequence
AX304425 Sequence
AX451838 Sequence
BD074012 Method fo
AR265212 Sequence
AX339688 Sequence
AX351768 Sequence
AX458824 Sequence
AR012146 Sequence
AR091248 Sequence
AR198283 Sequence
AR260437 Sequence
AR024460 Sequence
AR176004 Sequence
AR308620 Sequence
AR308639 Sequence
AR306692 Sequence
AX009400 Sequence
AX155549 Sequence
AX472252 Sequence
AX611465 Sequence
AX611467 Sequence
AX611469 Sequence
AX611470 Sequence
AX694371 Sequence
I63333 Sequence 14
A06347 oligonucleo
A94117 Sequence 98
AR232639 Sequence
AX011202 Sequence
AX327669 Sequence
AX452265 Sequence

AX230661 Sequence
AX488607 Sequence
I34244 Sequence 22
I34245 Sequence 21
A84028 Sequence 15
AR242538 Sequence
AX259784 Sequence
AX534164 Sequence
BD072705 Gene conv
AX054719 Sequence
S72525 TCR V gamma
A21836 Polynucleot
AX282986 Sequence
AX703532 Sequence
BD134517 Method fo
BD074024 Human gli
AR241103 Sequence
AR281777 Sequence
AX250715 Sequence
AX253315 Sequence
AX283518 Sequence
BD006136 Methods a
BD179019 A method
AX539255 Sequence
AX598275 Sequence
A31518 Synthetic H
AX207057 Sequence
AX534163 Sequence
AR008886 Sequence
AR087581 Sequence
BD012117 Vitamin D
BD080566 MFL ligand
I85137 Sequence 11
A75720 Sequence 10
BD133033 HM74 rece
I27338 Sequence 13
A84070 Sequence 5
AX107824 Sequence
E41514 Reporter ge
A68741 Sequence 3
AR016276 Sequence
AX003396 Sequence
AX118458 Sequence
AX328910 Sequence
AX339538 Sequence
AX503502 Sequence
BD086260 Vector. 8
BD177691 Process f
E12841 PCR primer
AR011576 Sequence
AR080447 Sequence
AR111511 Sequence
AR181111 Sequence
AX110734 Sequence
AX148786 Sequence
BD022388 Multi-fun
BD069819 Dendritic
I18214 Sequence 45
L07984 Bacterioph
A98445 Sequence 29
AR050289 Sequence
AR100579 Sequence
AR100585 Sequence
AR158965 Sequence
AR298667 Sequence
AR316120 Sequence
AR316177 Sequence
AX115823 Sequence
BD144090 Method fo
E26692 Improved me
I31522 Sequence 43
AR278808 Sequence

C 212	13.6	9.8	21	6	AX589272	AX589272 Sequence	C 285	13.4	9.6	25	6	AX501645	AX501645 Sequence
C 213	13.6	9.8	22	6	AX033204	AX033204 Sequence	C 286	13.4	9.6	25	6	AX501646	AX501646 Sequence
C 214	13.6	9.8	23	6	A61986	A61986 Sequence 16	C 287	13.4	9.6	25	6	AX501647	AX501647 Sequence
C 215	13.6	9.8	23	6	AX487068	AX487068 Sequence	C 288	13.4	9.6	25	6	AX534161	AX534161 Sequence
C 216	13.6	9.8	23	6	BD061613	BD061613 Human Laf	C 289	13.4	9.6	25	6	AX534162	AX534162 Sequence
C 217	13.6	9.8	24	6	AR095625	AR095625 Sequence	C 290	13.4	9.6	25	6	AX534166	AX534166 Sequence
C 218	13.6	9.8	24	6	AX106733	AX106733 Sequence	C 291	13.4	9.6	25	6	AX534517	AX534517 Sequence
C 219	13.6	9.8	24	6	AX446180	AX446180 Sequence	C 292	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 220	13.6	9.8	24	6	AX446782	AX446782 Sequence	C 293	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 221	13.6	9.8	24	6	AX683626	AX683626 Sequence	C 294	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 222	13.6	9.8	24	6	E49254	E49254 Omega 3 fat	C 295	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 223	13.6	9.8	25	6	A37998	A37998 Sequence 5	C 296	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 224	13.6	9.8	25	6	AR059422	AR059422 Sequence	C 297	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 225	13.6	9.8	25	6	AR285452	AR285452 Sequence	C 298	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 226	13.6	9.8	25	6	AR287486	AR287486 Sequence	C 299	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 227	13.6	9.8	25	6	AR307720	AR307720 Sequence	C 300	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 228	13.6	9.8	25	6	AX001355	AX001355 Sequence	C 301	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 229	13.6	9.8	25	6	AX534170	AX534170 Sequence	C 302	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 230	13.6	9.8	25	6	AX590588	AX590588 Sequence	C 303	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 231	13.6	9.8	25	6	BD000284	BD000284 cdna comp	C 304	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 232	13.6	9.8	25	6	I22220	I22220 Sequence 1	C 305	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 233	13.6	9.8	26	6	BD000254	BD000254 Oligonucl	C 306	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 234	13.6	9.8	26	6	BD000351	BD000351 Method fo	C 307	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 235	13.6	9.8	27	6	AR071913	AR071913 Sequence	C 308	13.4	9.6	26	6	AX037903	AX037903 Sequence
C 236	13.6	9.8	27	6	AR279431	AR279431 Sequence	C 309	13.4	9.6	26	6	AX037903	AX037903 Sequence
C 237	13.6	9.8	27	6	BD097281	BD097281 Novel col	C 310	13.4	9.6	27	6	AX090434	AX090434 Sequence
C 238	13.6	9.8	27	6	BD097291	BD097291 Novel col	C 311	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 239	13.6	9.8	28	6	AR198664	AR198664 Sequence	C 312	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 240	13.6	9.8	28	6	AX350231	AX350231 Sequence	C 313	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 241	13.6	9.8	28	6	AX350231	AX350231 Sequence	C 314	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 242	13.6	9.8	28	6	I62302	I62302 Sequence 13	C 315	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 243	13.6	9.8	29	6	AR221982	AR221982 Sequence	C 316	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 244	13.6	9.8	29	6	AX000864	AX000864 Sequence	C 317	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 245	13.6	9.8	29	6	AX304421	AX304421 Sequence	C 318	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 246	13.6	9.8	30	6	A51853	A51853 Sequence 17	C 319	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 247	13.6	9.8	30	6	A51857	A51857 Sequence 21	C 320	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 248	13.6	9.8	30	6	AR058826	AR058826 Sequence	C 321	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 249	13.6	9.8	30	6	AR125828	AR125828 Sequence	C 322	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 250	13.6	9.8	30	6	AR262364	AR262364 Sequence	C 323	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 251	13.6	9.8	30	6	AX028493	AX028493 Sequence	C 324	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 252	13.6	9.8	30	6	AX431446	AX431446 Sequence	C 325	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 253	13.6	9.8	30	6	B07788	B07788 PCR primer	C 326	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 254	13.6	9.8	30	6	I47240	I47240 Sequence 17	C 327	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 255	13.4	9.6	17	6	AX723714	AX723714 Sequence	C 328	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 256	13.4	9.6	18	6	AX352825	AX352825 Sequence	C 329	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 257	13.4	9.6	18	6	AX362670	AX362670 Sequence	C 330	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 258	13.4	9.6	18	12	AB069639	AB069639 Synthetic	C 331	13.4	9.6	28	6	AR109595	AR109595 Sequence
C 259	13.4	9.6	19	6	AX129291	AX129291 Sequence	C 332	13.4	9.6	28	6	AR109595	AR109595 Sequence
C 260	13.4	9.6	19	6	BD088226	BD088226 A method	C 333	13.4	9.6	28	6	AR109595	AR109595 Sequence
C 261	13.4	9.6	19	6	BD088226	BD088226 A method	C 334	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 262	13.4	9.6	19	6	BD088234	BD088234 A method	C 335	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 263	13.4	9.6	19	12	AB069137	AB069137 Synthetic	C 336	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 264	13.4	9.6	20	6	AR163797	AR163797 Synthetic	C 337	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 265	13.4	9.6	20	6	AR233647	AR233647 Sequence	C 338	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 266	13.4	9.6	21	6	E08711	E08711 Probe for d	C 339	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 267	13.4	9.6	22	6	AX742721	AX742721 Sequence	C 340	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 268	13.4	9.6	22	6	AX742722	AX742722 Sequence	C 341	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 269	13.4	9.6	23	6	AR037753	AR037753 Sequence	C 342	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 270	13.4	9.6	23	6	AR069386	AR069386 Sequence	C 343	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 271	13.4	9.6	23	6	AR081603	AR081603 Sequence	C 344	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 272	13.4	9.6	23	6	BD133242	BD133242 Polymaras	C 345	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 273	13.4	9.6	23	6	BD176902	BD176902 Gene enco	C 346	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 274	13.4	9.6	24	6	AX072270	AX072270 Sequence	C 347	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 275	13.4	9.6	24	6	AX089577	AX089577 Sequence	C 348	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 276	13.4	9.6	24	6	AX117886	AX117886 Sequence	C 349	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 277	13.4	9.6	24	6	AX327692	AX327692 Sequence	C 350	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 278	13.4	9.6	24	6	AX528500	AX528500 Sequence	C 351	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 279	13.4	9.6	24	6	E31858	E31858 Novel cance	C 352	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 280	13.4	9.6	24	6	I26381	I26381 Sequence 73	C 353	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 281	13.4	9.6	25	6	A27612	A27612 p150 Gene	C 354	13.4	9.6	29	6	AR109595	AR109595 Sequence
C 282	13.4	9.6	25	6	AR026123	AR026123 Sequence	C 355	13.4	9.6	29	6	AR109595	AR109595 Sequence
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AR163916 Sequence

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C 360	13.2	9.5	20	6	AX180379 Sequence	AX180379 Sequence	C 433	13.2	9.5	28	6	AR258737 Sequence	AR258737 Sequence
C 361	13.2	9.5	20	6	AX268920 Sequence	AX268920 Sequence	434	13.2	9.5	28	6	AX001136 Sequence	AX001136 Sequence
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C 365	13.2	9.5	20	6	BD011679 Method fo	BD011679 Method fo	C 438	13.2	9.5	28	6	AX092896 Sequence	AX092896 Sequence
C 366	13.2	9.5	20	6	BD011680 Method fo	BD011680 Method fo	C 439	13.2	9.5	28	6	BD085055 Laundry a	BD085055 Laundry a
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C 369	13.2	9.5	21	6	AR265767 Sequence	AR265767 Sequence	442	13.2	9.5	29	6	Al7444 oligonucleo	Al7444 oligonucleo
C 370	13.2	9.5	21	6	AR295668 Sequence	AR295668 Sequence	443	13.2	9.5	29	6	A23876 mutagenic o	A23876 mutagenic o
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C 373	13.2	9.5	21	6	AX555005 Sequence	AX555005 Sequence	446	13.2	9.5	29	6	AR061350 Sequence	AR061350 Sequence
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952 12.6 9.1 30 6 A18199
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954 12.6 9.1 30 6 AR016711
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959 12.6 9.1 30 6 AR065635
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961 12.6 9.1 30 6 AR095951
962 12.6 9.1 30 6 AR125785
963 12.6 9.1 30 6 AR135766
964 12.6 9.1 30 6 AR172584
965 12.6 9.1 30 6 AR243697
966 12.6 9.1 30 6 AR277826
967 12.6 9.1 30 6 AR279985
968 12.6 9.1 30 6 AR310549
969 12.6 9.1 30 6 AX001041
970 12.6 9.1 30 6 AX084314
971 12.6 9.1 30 6 AX135121
972 12.6 9.1 30 6 AX135122
973 12.6 9.1 30 6 AX233457
974 12.6 9.1 30 6 AX391534
975 12.6 9.1 30 6 AX463644
976 12.6 9.1 30 6 AX467222
977 12.6 9.1 30 6 AX494821
978 12.6 9.1 30 6 AX494862
979 12.6 9.1 30 6 AX536158
980 12.6 9.1 30 6 AX611466
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982 12.6 9.1 30 6 BD010272
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985 12.6 9.1 30 6 BD072802
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988 12.6 9.1 30 6 BD133155
989 12.6 9.1 30 6 BD136208
990 12.6 9.1 30 6 BD182091
991 12.6 9.1 30 6 BD182092
992 12.6 9.1 30 6 E27929
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994 12.6 9.1 30 6 I23528
995 12.6 9.1 30 6 I32404
996 12.6 9.1 30 6 I42198
997 12.6 9.1 30 6 I47197
998 12.6 9.1 30 6 I50069
999 12.6 9.1 30 6 I50070
1000 12.6 9.1 30 6 I50106
1001 12.6 9.1 30 6 I50107
1002 12.6 9.1 30 6 I50107

ALIGNMENTS
21 bp DNA linear PAT 27-AUG-2002
BD102270/c
LOCUS BD102270
DEFINITION Method of detecting risk factor for onset of arteriosclerosis.
ACCESSION BD102270
VERSION BD102270.1
KEYWORDS BD102270.1 GI:22647844
SOURCE WO 0171032-A/33.
ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Nagano,M., Ito,M., Sageshashi,Y., Hattori,H., Egashira,T.,
Yamashita,S. and Matsuzawa,Y.
Method of detecting risk factor for onset of arteriosclerosis
Patent: WO 0171032-A 33 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGESHASHI, HIROAKI HATTORI,
TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
OS Homo sapiens (human)
PN WO 0171032-A/33
PD 27-SEP-2001
PF 23-MAR-2001 WO 2001JP002327
PR 24-MAR-2000 JP OOP 084264
PI MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGESHASHI, HIROAKI HATTORI, TORU
EGASHIRA,
PI SHIZUYA YAMASHITA, YUJI MATSUZAWA
PC C12Q1/68,C12N15/12
CC Method of detecting risk factor for onset of arteriosclerosis
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'
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BASE COUNT 5 a 6 c 6 g 4 t
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Query Match 15.1%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 TCACAGCTGGACCCCTGGTGT 55
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Db 21 TCACAGCTGGACCCCTGGTGT 1
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RESULT 2
BX323474/c
LOCUS BX323474
DEFINITION Arabidopsis thaliana transposon insertion STS SM_3.36669, sequence
tagged site.
ACCESSION BX323474.1
VERSION BX323474.1 GI:29691536
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
1
REFERENCE
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
AUTHORS Clarke, J.H.
TITLE 2 (bases 1 to 30)
JOURNAL Direct Submission
COMMENT Submitted (08-APR-2003) Clarke, J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a
single line, Et an enhancer tag dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3' end of the
transposon. _5 denotes a sequence derived from the 5' end of the
transposon. BSRG GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N123380.
FEATURES
source
1..30
Location/Qualifiers

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CONTENTS

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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BASE COUNT
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Query Match
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 102 TTGGCTCCCACTCCCTCCT 121
Db 1 TTGGCTCCCACTCCCTCCT 20

RESULT 6
AR262363
LOCUS AR262363 30 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 1 from patent US 6323179.
ACCESSION AR262363
VERSION AR262363.1 GI:28073792
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Siler-Khodr, T.
TITLE Chicken GNRH analogs and uses thereof in regulation of fertility
JOURNAL Patent: US 6323179-A 1 27-NOV-2001;
FEATURES
source
1. .30
Location/Qualifiers
/organism="unknown"
BASE COUNT 5 a 8 c 9 g 8 t
ORIGIN

Query Match
Best Local Similarity 12.1%; Score 16.8; DB 6; Length 30;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 25 AGCACCAGGCTCACAGCTGGAACCTGG 52
Db 2 AGCACCAGGCTCACAGCTGGAACCTGG 29

RESULT 7
AR129513
LOCUS AR129513 22 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 102 from patent US 6187533.
ACCESSION AR129513
VERSION AR129513.1 GI:14117410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Bell, G.I., Yamagata, K., Oda, N., Kaisaki, P.J., Furuta, H.,
Horikawa, Y., and Menzel, S.
TITLE Mutations in the diabetes susceptibility genes hepatocyte nuclear
factor (HNF) 1 alpha (.alpha.), HNF1.beta. and HNF4.alpha
JOURNAL Patent: US 6187533-A 102 13-FEB-2001;
FEATURES
source
1. .22
Location/Qualifiers
/organism="unknown"
BASE COUNT 8 a 9 c 3 g 2 t
ORIGIN

Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 ACCAGGCTCACAGCTGGAAC 48
Db 2 ACCAGGCTCACAGCTGGAAC 22
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Db
|||||
2 ACCAGGCTCACAGCTGGAAC 22

RESULT 8
E24992/c
LOCUS E24992/c 28 bp DNA linear PAT 18-JUN-2001
DEFINITION Apoptosis-inhibiting protein, gene encoding the same and cDNA
theresol.
E24992
ACCESSION E24992
VERSION E24992.1 GI:13024690
KEYWORDS JP 1999116599-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 28)
AUTHORS Shigehiro, I. and Kenji, Y.
TITLE Apoptosis-inhibiting protein, gene encoding the same and cDNA
JOURNAL Patent: JP 1999116599-A 4 27-APR-1999;
COMMENT SCIENCE & TECH AGENCY
OS Unidentified
PN JP 1999116599-A/4
PD 27-APR-1999
PF 14-OCT-1997 JP 1997280831
PR SHIGEHIRO IKEDA, KENJI YAMAMOTO
PC C07K14/52, C07K16/28, C12N15/09, C12Q1/68, C12P21/02, (C12P21/02,
C12R1/19),
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source
1. .28
Location/Qualifiers
/organism="Unidentified"
FEATURES
source
1. .28
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 8 a 8 c 5 g 7 t
ORIGIN

Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 28;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CAGCGTGGTGGAGTTGGTT 82
Db 25 CAGCGTGGTGGAGTTGAATT 5

RESULT 9
AX597968/c
LOCUS AX597968/c 29 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 242 from Patent WO0244994.
ACCESSION AX597968
VERSION AX597968.1 GI:28398141
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
Neri, B.P., Reimer, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
Comerford, J., Stump, S. and Viegut, D.D.
TITLE Systems and method for detection assay production and sale
JOURNAL Patent: WO 0244994-A 242 06-JUN-2002;
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
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Best Local Similarity 85.7%; Pred. No. 4.1e+06;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 98 GAGATTCGGTCCCAACTCCTC 118
Db 27 GAAATTCCTCCCAACTCCTC 7

RESULT 10
LOCUS AR018179/c
DEFINITION Sequence 6 from patent US 5780611.
ACCESSION AR018179
VERSION AR018179.1 GI:3973782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 6 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
BASE COUNT      11 a      0 c      19 g      0 t
ORIGIN

Query Match      11.7%; Score 16.2; DB 6; Length 30;
Best Local Similarity 85.7%; Pred. No. 4e+06;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 106 CTCCCAACTCCTCCCTATCCT 126
Db 30 CTCCCTCCCTCCCTCTCTCTCT 10

RESULT 11
LOCUS AX180867/c
DEFINITION Sequence 15 from Patent WO0146691.
ACCESSION AX180867
VERSION AX180867.1 GI:15132696
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Joly,B.
TITLE A bioluminescence resonance energy transfer (bret) system with
broad spectral resolution between donor and acceptor emission
wavelengths and its use
JOURNAL Patent: WO 0146691-A 15 28-JUN-2001;
BioSignal Packard Inc. (CA)
FEATURES Location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT      7 a      9 c      12 g      2 t
ORIGIN

Query Match      11.7%; Score 16.2; DB 6; Length 30;
Best Local Similarity 72.4%; Pred. No. 4e+06;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 47 CCCTGGTGTCTCTCCAGCGGTGGGAG 75
Db 30 CCGGGTTCTCTCCCATGGTGGCGCTAG 2

RESULT 12
LOCUS E28689
DEFINITION Primer for detecting hepatitis B virus and method for detecting
hepatitis B virus therewith.
ACCESSION E28689
VERSION E28689.1 GI:13020850
KEYWORDS JP 1999262399-A/22.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Masakazu,M., Shuichi,K. and Kazumasa,H.
TITLE Primer for detecting hepatitis B virus and method for detecting
hepatitis B virus therewith
JOURNAL Patent: JP 1999262399-A 22 28-SEP-1999;
SRL-INC
COMMENT OS Unidentified
PN JP 1999262399-A/22
PD 28-SRP-1999
PF 17-MAR-1998 JP 1998087977
PR
PI MASAKAZU MUKAIDE, SHUICHI KANEKO, KAZUMASA HIKIJI PC
C1201/68, C07K14/02, C12Q1/70//C12N15/09, C12N15/00 CC Strandedness:
Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..25
/organism="Unidentified"
FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      1 a      7 c      6 g      9 t      2 others
ORIGIN

Query Match      11.5%; Score 16; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.8e+06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 42 TGGAACCTCGTCTCTCCTC 61
Db 5 TGGACCTTGTGKCTCCTC 24

RESULT 13
LOCUS A64642
DEFINITION Sequence 8 from Patent WO9731111.
ACCESSION A64642
VERSION A64642.1 GI:4530738
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Oude,E.R., Paulusma,C.C., Bosma,P.J., Borst,P., Evers,R., Kool and
Marcel.
TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING
THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM
JOURNAL Patent: WO 9731111-A 8 28-AUG-1997;
INTROGENE BV (NL)
COMMENT Other publication AU 1736697 19970910.
FEATURES Location/Qualifiers
source 1..26
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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BASE COUNT 4 a 9 c 6 g 7 t

Query Match 11.5%; Score 16; DB 6; Length 26;
Best Local Similarity 79.2%; Pred. No. 4.8e+06;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 29 CCAGGCTCAGCTGGACCTGG 52
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Db 2 CCAGGTTACATCTCGACTCTGG 25

RESULT 14

LOCUS AR009754/c 30 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 7 from patent US 5756448.

ACCESSION AR009754

VERSION AR009754.1 GI:3968559

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
Moore,D.D. and Baes,M.I.
TITLE Constitutive activator of retinoid (CAR) receptor polypeptides
JOURNAL Patent: US 5756448-A 7 26-MAY-1998;
FEATURES Location/Qualifiers
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source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGACCTGGTGTCTCTCCAG 64
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Db 30 TCAGGCTGCTGCTCTCTCTCTCTCCAG 1

RESULT 15

LOCUS I73485/c 30 bp DNA linear PAT 03-APR-1998

DEFINITION Sequence 7 from patent US 5686574.

ACCESSION I73485

VERSION I73485.1 GI:3009626

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
Moore,D.D. and Baes,M.I.
TITLE Constitutive activator of retinoid acid response (car) receptor fusion protein
JOURNAL Patent: US 5686574-A 7 11-NOV-1997;
FEATURES Location/Qualifiers
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source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGACCTGGTGTCTCTCCAG 64
|||||
Db 30 TCAGGCTGCTGCTCTCTCTCTCTCTCCAG 1

RESULT 16

LOCUS I84194/c 30 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 7 from patent US 5710017.

ACCESSION I84194

VERSION I84194.1 GI:3209484

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
Moore,D.D. and Baes,M.I.
TITLE DNA encoding a constitutive activator retinoic acid response (CAR) receptor
JOURNAL Patent: US 5710017-A 7 20-JAN-1998;
FEATURES Location/Qualifiers
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source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGACCTGGTGTCTCTCCAG 64
|||||
Db 30 TCAGGCTGCTGCTCTCTCTCTCTCTCCAG 1

RESULT 17

LOCUS AX081599 25 bp DNA linear PAT 27-FEB-2001

DEFINITION Sequence 104 from Patent WO0109350.

ACCESSION AX081599

VERSION AX081599.1 GI:13170424

KEYWORDS

SOURCE synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
Berthet,F.X., Dalemans,W.L., Denoel,P., Dequesne,G.S., Feron,C.S., Lobet,Y.S., Poolman,J.S., Thiry,G.S., Lhonnard,J.S. and Voet,P.S.,
Genetically engineered bleb vaccine
Patent: WO 0109350-A 104 08-FEB-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
LOCATION/Qualifiers
1..25
source

BASE COUNT 6 a 12 c 2 g 5 t

Query Match 11.1%; Score 15.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.5e+06;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 109 CCAACTCTCTCTATCTCTAAAGGCC 133
|||||
Db 1 CCAATCTCTCTCTCTCTAAAGGCC 25

RESULT 18

LOCUS AX374780 25 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 104 from Patent WO0209746.

ACCESSION AX374780

VERSION AX374780.1 GI:19169682

KEYWORDS

SOURCE synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1

Db 29 CTGGAGTCTCTGTGTCACCAACTGCAGC 5

RESULT 20
 AX323427
 LOCUS AX323427
 DEFINITION Sequence 19 from Patent WO0192578.
 ACCESSION AX323427
 VERSION AX323427.1 GI:18094190
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Roninson, I.B., Dokmanovic, M. and Chang, B.D.
 TITLE Regents and methods for identifying and modulating expression of genes regulated by retinoids
 JOURNAL Patent: WO 0192578-A 19 06-DEC-2001;
 Board of Trustees of the University of Illinois (US)
 FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="Antisense primer for beta IG-H3"
 6 a 7 c 3 g 4 t

BASE COUNT
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Query Match 10.9%; Score 15.2; DB 6; Length 20;
 Best Local Similarity 85.0%; Pred. No. 8.9e+06;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAAGCACCGGCTCAGCT 42
 DB 1 CATGCACAGGCTCATCT 20

RESULT 21
 AR142933
 LOCUS AR142933
 DEFINITION Sequence 19 from patent US 6204025.
 ACCESSION AR142933
 VERSION AR142933.1 GI:15104219
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Liu, Q.
 TITLE Efficient linking of nucleic acid segments
 JOURNAL Patent: US 6204025-A 19 20-MAR-2001;
 FEATURES
 Location/Qualifiers
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 /organism="unknown"
 8 a 2 c 10 g 3 t

BASE COUNT
 ORIGIN

Query Match 10.9%; Score 15.2; DB 6; Length 23;
 Best Local Similarity 85.0%; Pred. No. 8.7e+06;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 83 AGGAGTACGGAGATGGAGAT 102
 DB 4 AGGAGGAGGAGATGGACAT 23

RESULT 22
 AR277835
 LOCUS AR277835
 DEFINITION Sequence 24 from patent US 6511802.
 ACCESSION AR277835
 VERSION AR277835.1 GI:29711759

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Albrecht, G., Brenner, S. and Dubridge, R.B.
  TITLE
  Solid phase screening of differentially expressed genes
  JOURNAL
  Patent: US 651802-A 24 28-JAN-2003;
FEATURES
  source
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  /db_xref="taxon:32630"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
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Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTGTC 56
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Db      6 ACAGCTGCATCCCTGGTGTGAC 25

RESULT 23
AR279994
LOCUS      AR279994      30 bp      DNA      linear      PAT 10-APR-2003
DEFINITION      Sequence 26 from patent US 6518023.
ACCESSION      AR279994
VERSION      AR279994.1 GI:29715183
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Brenner, S.
  TITLE
  Method of mapping restriction sites in polynucleotides
  JOURNAL
  Patent: US 6518023-A 26 11-FEB-2003;
FEATURES
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  /organism="unknown"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGTGAC 25

RESULT 24
BD128452
LOCUS      BD128452      30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION      Solid phase screening of differentially expressed genes.
ACCESSION      BD128452
VERSION      BD128452.1 GI:23223397
KEYWORDS      JP 2002500050-A/24.
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Albrecht, G., Brenner, S. and Dubridge, R.
  TITLE
  Solid phase screening of differentially expressed genes
  JOURNAL
  Patent: JP 2002500050-A 24 08-JAN-2002;
  LYNX THERAPEUTICS INC
COMMENT
  OS Artificial Sequence
  PN JP 2002500050-A/24
  PD 08-JAN-2002
  PF 08-JAN-1999 JP 2000527674
  PR 09-JAN-1998 US 09/005222, 06-AUG-1998 US 09/130446 PI
  GLENN ALBRECHT, SYDNEY BRENNER, ROBERT DUBRIDGE PC

C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Synthetic CC n can be a
or g or c or t
CC n can be a or g or c or t
FH Key Location/Qualifiers
FT misc_difference (1)..(2)
FT misc_difference (4).
  Location/Qualifiers
  1..30
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTGTC 56
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Db      6 ACAGCTGCATCCCTGGTGTGAC 25

RESULT 25
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DEFINITION      Method of mapping restriction sites in polynucleotides.
ACCESSION      BD133164
VERSION      BD133164.1 GI:23228109
KEYWORDS      JP 2002507126-A/26.
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Brenner, S.
  TITLE
  Method of mapping restriction sites in polynucleotides
  JOURNAL
  Patent: JP 2002507126-A 26 05-MAR-2002;
  LYNX THERAPEUTICS INC
COMMENT
  EN JP 2002507126-A/26
  PD 05-MAR-2002
  PF 25-JUN-1998 JP 1999505776
  PR 27-JUN-1997 US 08/894189
  PI SYDNEY BRENNER
  PC C12Q1/68
  CC Strandedness: Double;
  CC Topology: Linear;
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  /mol_type="genomic DNA"
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BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGTGAC 25

Search completed: August 22, 2003, 10:37:12
Job time : 1668 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      August 22, 2003, 08:41:19 ; Search time 170 Seconds
              (without alignments)
              2207.188 Million cell updates/sec

Title:      US-09-925-139-3_COPY_1631_1769
Perfect score: 139
Sequence:    1 ggatggggctttagcagaa.....ctatcctaaagccactgg 139

Scoring table:  IDENTITY NUC
                  Gapop 10.0 , Gapext 1.0

Searched:      2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:      2101872

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
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                  Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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SUMMARIES

Result No.	Query			Length	DB	ID	Description
	Score	Match	%				
C 1	21	15	1	21	22	AAI66686	Human CERP DNA rel
C 2	20	14	4	20	24	ABT13031	Human cholesterol
C 3	20	14	4	20	25	ABX12175	Human cholesterol
C 4	20	14	4	20	25	ABX12198	Human cholesterol
C 5	20	14	4	20	25	ABX12199	Human cholesterol
C 6	20	14	4	20	25	ABX12200	Human cholesterol
C 7	20	14	4	20	25	ABX12217	Human cholesterol
C 8	20	14	4	20	25	ABX12218	Human cholesterol

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	9	20	14.4	20	25	ABX13219	Human cholesterol
C	10	20	14.4	20	25	ABX13220	Human cholesterol
C	11	18	12.9	18	17	ANT50642	Human CETP hairpin
C	12	17.2	12.4	22	20	AAX37644	HBV detecting prim
C	13	17	12.2	17	20	AAX22550	Human CETP RNA fra
C	14	16.8	12.1	21	24	AAX199829	Human G protein-co
C	15	16.8	12.1	27	20	AAX21403	T.ni acyl-CoA deht
C	16	16.8	12.1	30	22	AAS14772	Chicken li gonadot
C	17	16.8	12.1	30	24	AAD46973	Chicken gonadotrop
C	18	16.8	12.1	30	24	ABK47482	DNA encoding chick
C	19	16.4	11.8	29	21	AAO44239	Polymorphic fragme
C	20	16.4	11.8	30	25	ACC46916	Mouse phospholipas
C	21	16.2	11.7	22	19	AAV52705	Hepatocyte nuclear
C	22	16.2	11.7	28	20	AAX56275	Human neuronal apo
C	23	16.2	11.7	30	18	AAT60157	Collagen gene prom
C	24	16.2	11.7	30	21	AAZ98705	Collagen promoter
C	25	16	11.5	25	20	AAX27655	HBV genomic DNA fr
C	26	16	11.5	25	20	AAX27655	PCR primer'4 used
C	27	16	11.5	26	18	ABX94031	Human NOV-associat
C	28	16	11.5	26	24	ABX97568	Bacillus sp. pecti
C	29	16	11.5	29	19	AAX59490	17x. AccX Primer
C	30	16	11.5	29	17	AAT38183	20x. ApalX Primer
C	31	16	11.5	29	17	AAT38187	22x. AfIX Primer
C	32	16	11.5	29	17	AAT38189	9x. SgrX Primer
C	33	16	11.5	29	17	AAT38193	11x. XbaX Primer
C	34	16	11.5	29	17	AAT38167	12x. BamX Primer
C	35	16	11.5	29	17	AAT38171	14x. NotX Primer
C	36	16	11.5	29	17	AAT38173	4x. HinX Primer
C	37	16	11.5	29	17	AAT38177	7x. NcoX Primer
C	38	16	11.5	29	17	AAT38157	10x. AscX Primer
C	39	16	11.5	30	17	AAT38169	1x. EcoX Primer
C	40	16	11.5	30	17	AAT38151	Novel Helicobacter
C	41	15	11.5	30	24	ABX67898	Mouse p97 (mp97) c
C	42	15.8	11.4	29	22	AAD14471	Human CD33-like pr
C	43	15.8	11.4	30	19	AAX25984	Human zinc finger
C	44	15.6	11.2	24	24	ABZ57102	Rat alpha-myosin h
C	45	15.6	11.2	30	14	AAQ46137	Rat alpha-myosin h
C	46	15.6	11.2	30	20	AAX24000	N. meningitidis Po
C	47	15.4	11.1	25	22	ABF91478	Promoter replaceme
C	48	15.4	11.1	25	24	ABK37858	Human H11 coding s
C	49	15.4	11.1	26	22	AAF74325	GPCR protein BG37
C	50	15.4	11.1	29	24	ABL54487	Antisense primer,
C	51	15.2	10.9	20	24	AAD24930	P9 gene PCR primer
C	52	15.2	10.9	23	20	AAX30209	Encoded adaptor se
C	53	15.2	10.9	30	19	AAV16704	DNA-tag used to ta
C	54	15.2	10.9	30	20	AAO3323	Adaptor #15 used i
C	55	15.2	10.9	30	21	AAZ92118	Human CETP HH ribo
C	56	15	10.8	15	17	AAT49815	Human CETP HH ribo
C	57	15	10.8	15	17	AAT49817	Human CETP HH ribo
C	58	15	10.8	15	17	AAT49819	Human CETP HH ribo
C	59	15	10.8	15	17	AAT49821	Human CETP HH ribo
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C	72	15	10.8	15	17	AAT49813	Human POSHL1 scann
C	73	15	10.8	15	22	AAD04591	Human POSHL1 scann
C	74	15	10.8	25	24	ABV92961	BRCA2 cancer suscep
C	75	15	10.8	25	24	ABV92963	PCR primer for DNA
C	76	15	10.8	26	18	AAV92592	Human cytokine rec
C	77	15	10.8	29	21	AAA75566	Human zalfphall rec
C	78	15	10.8	29	24	AAS20665	Human soluble zalp
C	79	15	10.8	29	24	AAS20665	
C	80	15	10.8	29	24	AAS20665	
C	81	15	10.8	29	24	AAD22930	

C 82	15	10.8	30	16	AAQ89012	VEGF 2'-NH2-RNA nu
C 83	14.8	10.6	20	24	ABSG60987	Human genotyping P
C 84	14.8	10.6	22	22	AAH28671	Human interleukin-
C 85	14.8	10.6	25	22	AA161997	Soybean 2400L7 reg
C 86	14.8	10.6	26	22	AAH78617	PCR primer Bx2Dn(2
C 87	14.8	10.6	27	16	AAU04690	Black widow spider
C 88	14.8	10.6	27	24	AAK99801	Bacillus sp alkali
C 89	14.8	10.6	30	15	AAQ67087	CHC-2 primer. Syn
C 90	14.8	10.6	30	21	AAZ88251	Treponea pallidum
C 91	14.8	10.6	30	22	AAK60081	Primer #5 for gene
C 92	14.6	10.5	21	21	AAK36969	Human dysferlin ex
C 93	14.6	10.5	21	21	AAAL1514	Human dysferlin ex
C 94	14.6	10.5	24	22	AAH45241	Human rhoc PCR pri
C 95	14.6	10.5	24	24	AAU50713	Pseudomonas glutar
C 96	14.6	10.5	24	24	AAH18863	Growth hormone 1 g
C 97	14.6	10.5	24	24	AB189890	Capture oligonucle
C 98	14.6	10.5	24	24	AB189891	Capture oligonucle
C 99	14.6	10.5	25	24	ABV92964	Human POSHL1 scann
C 100	14.6	10.5	25	24	ABV92965	Human POSHL1 scann
C 101	14.6	10.5	27	24	AAU50701	Pseudomonas glutar
C 102	14.6	10.5	29	18	AAU45117	Cytomegalovirus po
C 103	14.6	10.5	29	21	AAAO4246	Polymorphic fragme
C 104	14.6	10.5	30	17	AAU41675	Endo-xyloglucan tr
C 105	14.6	10.5	30	20	AA223514	T cell receptor V
C 106	14.6	10.5	30	24	ABK15255	Hepatitis B virus
C 107	14.4	10.4	18	24	ABU58444	CYP-C probe genera
C 108	14.4	10.4	20	24	ABZ31506	Candida albicans G
C 109	14.4	10.4	20	24	ABV73609	S. albulus plasmid
C 110	14.4	10.4	20	24	AB193783	Capture oligonucle
C 111	14.4	10.4	21	24	ABQ93591	Human DISC1/DIS2
C 112	14.4	10.4	24	20	AAZ40497	Degenerate primer
C 113	14.4	10.4	24	21	AAAO8873	5' RACE primer for
C 114	14.4	10.4	24	21	AAAO8876	Nested 3' RACE pri
C 115	14.4	10.4	24	22	AAO8718	Forward PCR primer
C 116	14.4	10.4	24	22	AAO41190	A. niger LLP-2 C-
C 117	14.4	10.4	24	24	ABQ00835	Oligonucleotide ad
C 118	14.4	10.4	24	24	ABQ05632	Oligonucleotide ad
C 119	14.4	10.4	24	24	ABQ05673	Oligonucleotide ad
C 120	14.4	10.4	24	24	AB184137	Capture oligonucle
C 121	14.4	10.4	25	21	AAAF3218	Capture oligonucle
C 122	14.4	10.4	25	22	AAAF54325	Primer #48 used in
C 123	14.4	10.4	25	24	AAAL1088	Small acid-soluble
C 124	14.4	10.4	25	24	ABN11290	Human GMPLP-1 25-m
C 125	14.4	10.4	25	24	ABN11291	Primer used when o
C 126	14.4	10.4	26	18	AAV06178	Primer 1 for human
C 127	14.4	10.4	26	21	AAAF4718	Human PDE10A 5' RA
C 128	14.4	10.4	26	22	ABAO3666	Human genomic DNA
C 129	14.4	10.4	26	24	ABD39292	Human gene specifi
C 130	14.4	10.4	26	24	ABK65554	Human gene specifi
C 131	14.4	10.4	26	24	ABK65562	Bacillus sp. pecti
C 132	14.4	10.4	27	19	AAV59485	Bacillus sp. pecti
C 133	14.4	10.4	27	19	AAV59491	P450RAI-2 polypt
C 134	14.4	10.4	27	22	AAH22440	Human cytochrome P
C 135	14.4	10.4	27	24	ABQ74191	Primer for DNA enc
C 136	14.4	10.4	28	22	AAH77658	Sense PCR primer i
C 137	14.4	10.4	28	22	AAH45591	Phagemid vector pc
C 138	14.4	10.4	28	22	AAAF82467	Oligonucleotide #1
C 139	14.4	10.4	28	22	AAAD03560	Rat secreted facto
C 140	14.4	10.4	28	24	AAAS94738	Blocking oligonuc
C 141	14.4	10.4	29	25	ABV76930	HBV amplifier prob
C 142	14.4	10.4	30	14	AAQ45815	PCR primer for HSV
C 143	14.4	10.4	30	15	AAQ73656	PC receptor PCR pr
C 144	14.4	10.4	30	16	AAQ86854	Herbicide-resistan
C 145	14.4	10.4	30	18	AAAT62737	Ovine IL-12 35 kD
C 146	14.4	10.4	30	18	AAAT50765	Chimeric FcgammaRI
C 147	14.4	10.4	30	19	AAV56028	Chimeric FcgammaRI
C 148	14.4	10.4	30	19	AAV56029	HBV.84 amplifier p
C 149	14.4	10.4	30	19	AAV07812	Amplifier probe HB
C 150	14.4	10.4	30	20	AAV83041	HSV-2 gH gene PCR
C 151	14.4	10.4	30	20	AAV64106	Human PC receptor
C 152	14.4	10.4	30	21	AAAG0012	PCR primer 1b for
C 153	14.4	10.4	30	25	ABX15171	
C 154	14.4	10.4	30	25	ABX15172	
C 155	14.4	10.4	30	25	ABX15172	PCR primer 2a for
C 156	14.2	10.2	20	16	AAO82244	Hepatitis B virus
C 157	14.2	10.2	20	16	AAQ81567	Europium (III) tex
C 158	14.2	10.2	20	16	AAQ80879	Europium (III) tex
C 159	14.2	10.2	20	16	AAQ80880	Dysprosium (III) t
C 160	14.2	10.2	20	16	AAQ91455	Oligonucleotide #4
C 161	14.2	10.2	20	19	AAV07290	Texaphyrin oligonu
C 162	14.2	10.2	20	19	AAV07037	Antisense primer f
C 163	14.2	10.2	20	20	AAV92122	Exemplary texaphyr
C 164	14.2	10.2	20	21	AAZ88439	Human diacylglycer
C 165	14.2	10.2	20	22	AAAD05958	Human RCOL2 antis
C 166	14.2	10.2	20	24	AAAD1746	Stabilising reagen
C 167	14.2	10.2	20	25	ABT23628	HPV-16, synthetic
C 168	14.2	10.2	22	24	ABK14592	mRNA target probe.
C 169	14.2	10.2	25	15	AAQ55871	Probe for the den
C 170	14.2	10.2	25	16	AAQ85287	Probe used for det
C 171	14.2	10.2	25	20	AAAX05283	Goose malonyl CoA
C 172	14.2	10.2	26	21	AAZ87691	ICE-LAP-1 5' PCR p
C 173	14.2	10.2	27	17	AAAT15580	Human BUB1B kinase
C 174	14.2	10.2	27	20	AAAX58976	Human synaptotomal
C 175	14.2	10.2	27	20	AAAX24682	PCR primer PDM-208
C 176	14.2	10.2	27	20	AAAX58976	PCR primer for SCP
C 177	14.2	10.2	27	22	AAH38915	Human SCP-1 RT-PCR
C 178	14.2	10.2	27	22	AAH39363	SNP specific SNPE
C 179	14.2	10.2	27	22	AAH61713	SNP specific SNPE
C 180	14.2	10.2	27	22	ABK69866	Human CTAGE-1 PCR
C 181	14.2	10.2	27	24	ABQ75497	Ehrlichia antigen
C 182	14.2	10.2	27	24	ABK69866	Mouse epididymal p
C 183	14.2	10.2	27	24	ABQ75497	Human tumour marke
C 184	14.2	10.2	27	24	ABK69866	Human granulocyte
C 185	14.2	10.2	27	24	ABK69866	R. marinus Cell2A
C 186	14.2	10.2	28	24	ABAO0500	Truncated cellulas
C 187	14.2	10.2	28	24	ABAO0500	Immunostimulatory
C 188	14.2	10.2	28	24	ABAO0500	Human G-protein co
C 189	14.2	10.2	28	24	ABAO0500	Primer HTLCA-R for
C 190	14.2	10.2	28	24	ABAO0500	Primer HTLCA-R for
C 191	14.2	10.2	28	24	ABAO0500	PCR primer HTLCA-R
C 192	14.2	10.2	28	24	ABAO0500	Polymorphic fragme
C 193	14.2	10.2	29	21	AAK04539	Human gene specifi
C 194	14.2	10.2	29	21	ABK67280	PCR primer for hum
C 195	14.2	10.2	30	15	AAQ73546	Insulin beta-chain
C 196	14.2	10.2	30	18	AAV55241	Primer for human m
C 197	14.2	10.2	30	19	AAV54148	Nucleotide sequenc
C 198	14.2	10.2	30	19	AAV41926	DNA encoding a HRG
C 199	14.2	10.2	30	20	AAAX27664	Human Egr-1 promot
C 200	14.2	10.2	30	21	AAZ39731	Human Egr-1 promot
C 201	14.2	10.2	30	22	AAFP0458	Extended primer us
C 202	14.2	10.2	30	22	AAFP0458	Novel Helicobacter
C 203	14.2	10.2	30	24	ABX68589	PCR primer kbg381
C 204	14.2	10.2	30	24	ABX68589	HRGP related oligo
C 205	14.2	10.2	30	24	ABX68589	Hydroxyproline-ric
C 206	14.2	10.2	30	24	ABX68589	Hydroxyproline-ric
C 207	14.2	10.2	30	24	ABX68589	Hydroxyproline Gly
C 208	14.2	10.2	30	24	ABX68589	Oct-4 transcript R
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C 210	14.2	10.2	30	21	AAAS8421	Lactococcus lactis
C 211	14.2	10.2	30	22	AAAS8421	Forward PCR prim
C 212	14.2	10.2	30	22	AAAS8421	Nurri mRNA PCR pri
C 213	14.2	10.2	30	22	AAAS8421	Yeast PCR primer S
C 214	14.2	10.2	30	22	AAAS8421	PCR primer for clo
C 215	14.2	10.2	30	22	AAAS8421	PCR primer for clo
C 216	14.2	10.2	30	22	AAAS8421	Retroviral DNA bas
C 217	14.2	10.2	30	22	AAAS8421	Urease gene antis
C 218	14.2	10.2	30	22	AAAS8421	Candida albicans G
C 219	14.2	10.2	30	22	AAAS8421	Capture oligonucle
C 220	14.2	10.2	30	22	AAAS8421	Penicillium chrys
C 221	14.2	10.2	30	22	AAAS8421	Primer for micros
C 222	14.2	10.2	30	22	AAAS8421	Afx transcription
C 223	14.2	10.2	30	22	AAAS8421	Human POSHL1 scann
C 224	14.2	10.2	30	22	AAAS8421	
C 225	14.2	10.2	30	22	AAAS8421	
C 226	14.2	10.2	30	22	AAAS8421	
C 227	14.2	10.2	30	22	AAAS8421	

C 374	13.6	9.8	30	21	AAAT2673	PCR primer R1 used	C 447	13.4	9.6	26	16	AAQ920619	B amyloidoliquefacien
C 375	13.6	9.8	30	22	AAAT2673	Salmon gonadotropin	C 448	13.4	9.6	26	20	AAZ06719	Primer for the sit
C 376	13.6	9.8	30	22	AAAT2673	Herring gonadotropin	C 449	13.4	9.6	26	22	AAZ06719	Primer Ag80(R) emp
C 377	13.6	9.8	30	22	AAAT2673	2'NH2 RNA ligand t	C 450	13.4	9.6	26	22	AAZ06719	Information carryi
C 378	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 451	13.4	9.6	26	22	AAZ06719	Degenerate primer
C 379	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 452	13.4	9.6	27	17	AAZ06719	G-protein coupled
C 380	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 453	13.4	9.6	27	17	AAZ06719	Galanin receptor D
C 381	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 454	13.4	9.6	27	17	AAZ06719	Cytosactin PCR pri
C 382	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 455	13.4	9.6	27	18	AAZ06719	Receptor protein d
C 383	13.6	9.8	30	24	ABX68590	Novel Helicobacter	C 456	13.4	9.6	27	18	AAZ06719	Primer #2 for G pr
C 384	13.6	9.8	30	25	ABZ58508	Fat regulated gene	C 457	13.4	9.6	27	20	AAZ06719	G protein-coupled
C 385	13.6	9.8	30	25	ABZ58508	DNA encoding salmo	C 458	13.4	9.6	27	20	AAZ06719	Mouse APO4-alpha R
C 386	13.6	9.8	30	25	ABZ58508	Transmembrane seri	C 459	13.4	9.6	27	20	AAZ06719	Probe used to scre
C 387	13.4	9.6	18	14	AAQ50940	DNA sequence 1. U	C 460	13.4	9.6	27	20	AAZ06719	Human G-protein co
C 388	13.4	9.6	18	14	AAQ50940	DNA sequence 2. U	C 461	13.4	9.6	27	22	AAZ06719	Imperfect direct r
C 389	13.4	9.6	19	21	AAH88809	T-cell antigen rec	C 462	13.4	9.6	27	22	AAZ06719	Imperfect direct r
C 390	13.4	9.6	19	21	AAH88809	Hiv-1 related bind	C 463	13.4	9.6	27	22	AAZ06719	Imperfect direct r
C 391	13.4	9.6	19	22	AAH88809	cdk4 ribozyme bind	C 464	13.4	9.6	27	22	AAZ06719	PCR primer used to
C 392	13.4	9.6	19	24	ABL43426	Primer to amplify	C 465	13.4	9.6	27	24	ABK66466	Human 23kDa highly
C 393	13.4	9.6	19	24	ABL43426	Cell-cycle depende	C 466	13.4	9.6	27	24	ABK66466	Human gene speci
C 394	13.4	9.6	19	24	ABL43426	Human chromosome 1	C 467	13.4	9.6	27	24	ABK66466	Oligonucleotide JC
C 395	13.4	9.6	20	22	AAZ06719	Human chromosome 1	C 468	13.4	9.6	27	24	ABK66466	3'-5' sequence of
C 396	13.4	9.6	20	22	AAZ06719	Human cytohesin-2	C 469	13.4	9.6	27	24	ABK66466	Human ligand (1-60
C 397	13.4	9.6	21	14	AAQ49142	Human ATM gene exo	C 470	13.4	9.6	27	24	ABK66466	Human tumour vascu
C 398	13.4	9.6	21	14	AAQ49142	Human IFNGR2 antis	C 471	13.4	9.6	27	24	ABK66466	Galanin-like pepti
C 399	13.4	9.6	21	16	AAQ88865	A. pleuropneumonia	C 472	13.4	9.6	28	24	ABT08471	Reproductive recom
C 400	13.4	9.6	21	17	AAZ35044	A. pleuropneumonia	C 473	13.4	9.6	28	24	ABT08471	Human liver activi
C 401	13.4	9.6	21	17	AAZ35044	Actinobacillus ple	C 474	13.4	9.6	29	19	AAV38259	Human liver activi
C 402	13.4	9.6	21	17	AAZ35044	HBV target (positi	C 475	13.4	9.6	29	19	AAV38259	Human secreted pro
C 403	13.4	9.6	22	18	AAZ76127	HBV DR region frag	C 476	13.4	9.6	29	21	AAZ50604	3' VITR66BpE1 pri
C 404	13.4	9.6	22	18	AAZ76127	Human eosinophil m	C 477	13.4	9.6	29	21	AAZ50604	Potential antisens
C 405	13.4	9.6	22	21	AAZ33830	Human major basic	C 478	13.4	9.6	29	22	AAH19363	PCR primer #6. Un
C 406	13.4	9.6	22	21	AAZ33830	Low adenosine anti	C 479	13.4	9.6	29	22	AAH19363	BMP-8 protein prob
C 407	13.4	9.6	22	21	AAZ33830	Low adenosine anti	C 480	13.4	9.6	30	12	ABQ15241	Primer 3FU for IGE
C 408	13.4	9.6	23	14	AAQ36379	GP11a antisense p	C 481	13.4	9.6	30	12	ABQ15241	Human PLAP gene sp
C 409	13.4	9.6	23	14	AAQ36379	Telomerase m1matc	C 482	13.4	9.6	30	12	ABQ15241	Human V3 loop HIV
C 410	13.4	9.6	23	18	AAZ6380	Human alpha-1 anti	C 483	13.4	9.6	30	12	ABQ15241	Human G protein-co
C 411	13.4	9.6	23	18	AAZ6380	Sense PCR primer f	C 484	13.4	9.6	30	12	ABQ15241	5' PCR primer to o
C 412	13.4	9.6	23	20	AAZ28446	21-hydroxylase int	C 485	13.4	9.6	30	12	ABQ15241	Sequence of PCR pr
C 413	13.4	9.6	23	20	AAZ28446	Arabidopsis thalia	C 486	13.4	9.6	30	12	ABQ15241	Antifungal agent s
C 414	13.4	9.6	23	24	ABZ54975	Nucleotide sequenc	C 487	13.4	9.6	30	24	ABX03633	Human VEGF-D CDNA
C 415	13.4	9.6	23	24	ABZ54975	Type II procollage	C 488	13.4	9.6	30	24	ABX03633	Novel Helicobacter
C 416	13.4	9.6	24	21	AAZ64562	PCR primer for amp	C 489	13.4	9.6	30	24	ABX03633	Human aurora 2 pro
C 417	13.4	9.6	24	21	AAZ64562	Reverse PCR primer	C 490	13.4	9.6	30	24	ABX03633	Human vitamin D3 r
C 418	13.4	9.6	24	21	AAZ64562	Engrailed mRNA PCR	C 491	13.4	9.6	30	24	ABX03633	Human VEGF-D PCR p
C 419	13.4	9.6	24	21	AAZ64562	Human neuromedin B	C 492	13.4	9.6	30	24	ABX03633	Human G protein-co
C 420	13.4	9.6	24	22	AAH40213	SNP specific upper	C 493	13.4	9.6	30	24	ABX03633	Petunia chalcone i
C 421	13.4	9.6	24	24	ABV72780	Chimeric antisense	C 494	13.4	9.6	30	24	ABX03633	Collagen gene prom
C 422	13.4	9.6	24	24	ABV72780	Human B7 related p	C 495	13.4	9.6	30	24	ABX03633	Antisense oligonuc
C 423	13.4	9.6	24	24	ABV72780	GTP protein activa	C 496	13.4	9.6	30	24	ABX03633	Smad2 antisense ol
C 424	13.4	9.6	24	24	ABV72780	Honeodomain trans	C 497	13.2	9.5	18	21	AAA10567	Collagen promoter
C 425	13.4	9.6	25	13	AAQ22227	3' PCR primer for	C 498	13.2	9.5	18	21	AAA10567	Antisense oligo, I
C 426	13.4	9.6	25	16	AAQ22227	Primer M3 which co	C 499	13.2	9.5	18	21	AAA10567	Human SRC-1 antis
C 427	13.4	9.6	25	20	AAZ98187	Human NARC protein	C 500	13.2	9.5	18	21	AAA10567	Mouse MP-1 antis
C 428	13.4	9.6	25	22	AAH74301	PCR primer for nuc	C 501	13.2	9.5	18	21	AAA10567	Human chromosome 1
C 429	13.4	9.6	25	22	AAH74301	Soybean 240017 reg	C 502	13.2	9.5	18	21	AAA10567	Dysprosium (III) t
C 430	13.4	9.6	25	22	AAH74301	Protein kinase CDN	C 503	13.2	9.5	18	21	AAA10567	Metallotexaphyrin
C 431	13.4	9.6	25	24	ABV81706	Human HTPL scannin	C 504	13.2	9.5	18	24	ABX3557	Human tankyrase II
C 432	13.4	9.6	25	24	ABV81706	Human HTPL scannin	C 505	13.2	9.5	18	24	ABX3557	A allele probe VP6
C 433	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 506	13.2	9.5	19	16	AAQ91454	Primer #4 for ente
C 434	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 507	13.2	9.5	19	16	AAQ91454	Calcium ion channe
C 435	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 508	13.2	9.5	19	16	AAQ91454	PCR primer used to
C 436	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 509	13.2	9.5	19	16	AAQ91454	PI3K antisense inh
C 437	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 510	13.2	9.5	20	13	AAQ29803	Mouse GAPDH PCR pr
C 438	13.4	9.6	25	24	ABV81706	Human POSHL1 scann	C 511	13.2	9.5	20	13	AAQ29803	16S/23S rRNA spacer
C 439	13.4	9.6	25	24	ABV81706	Human NOV9 exon 11	C 512	13.2	9.5	20	17	AAZ39874	Primer JN14 to is
C 440	13.4	9.6	25	24	ABV81706	Hominidae LDL rece	C 513	13.2	9.5	20	19	AAV29418	Human hepsin antis
C 441	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 514	13.2	9.5	20	21	AAZ13141	Human hepsin antis
C 442	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 515	13.2	9.5	20	21	AAZ13141	
C 443	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 516	13.2	9.5	20	22	AAI69777	
C 444	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 517	13.2	9.5	20	22	AAI69777	
C 445	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 518	13.2	9.5	20	24	AAZ40662	
C 446	13.4	9.6	25	24	ABV81706	Human GMPLP-1 25-m	C 519	13.2	9.5	20	24	AAZ40662	

520	13.2	9.5	20	24	ABL94348	Mouse C/EBP beta p	13.2	9.5	26	25	ABX81167	Human secreted or
521	13.2	9.5	20	25	ABZ37372	Kappa light chain	13.2	9.5	26	25	ABX90257	Human secreted/tra
522	13.2	9.5	21	16	AAZ04956	Upstream primer fo	13.2	9.5	26	25	ABX77868	Human PRO PCR prim
523	13.2	9.5	21	19	AAZ28664	Human polymorphic	13.2	9.5	26	25	ABX79464	Human secreted/tr
524	13.2	9.5	21	19	AAV33397	PCR primer MABCR1R	13.2	9.5	26	25	ABX64103	Human PRO DNA PCR
525	13.2	9.5	21	21	AAZ73047	Human biallelic ma	13.2	9.5	26	25	ABX17067	Human PRO PCR prim
526	13.2	9.5	21	21	AAA72338	Human RecQ4 helica	13.2	9.5	27	18	AAT89777	Plasmid pET-E2.123
527	13.2	9.5	21	21	AAZ92708	Rous sarcoma virus	13.2	9.5	27	18	AAT88237	Primer EA21 for BP
528	13.2	9.5	21	22	AAZ96342	Human gene single	13.2	9.5	27	18	AAT84579	Tat-E2 conjugate p
529	13.2	9.5	21	22	ABZ98164	Human multdrug re	13.2	9.5	27	19	AAV98790	Human EGF-R hamme
530	13.2	9.5	21	24	ABZ98398	Human TIMP-1 promo	13.2	9.5	27	19	AAV96930	Human EGF-R hamme
531	13.2	9.5	21	24	ABZ98425	Human TIMP-1 promo	13.2	9.5	27	19	AAV96930	Potato citrate syn
532	13.2	9.5	21	24	ABK00012	Rous sarcoma virus	13.2	9.5	27	19	AAV56609	TAT-E2 conjugate p
533	13.2	9.5	21	24	ABK98414	Mouse glyceraldehy	13.2	9.5	27	20	AAV60284	PCR primer used to
534	13.2	9.5	21	25	ABK98975	Human AAGA SNP ana	13.2	9.5	27	20	AAV57514	Preneilin binding
535	13.2	9.5	22	18	AAT85771	PMR2 gene PCR prim	13.2	9.5	27	22	AAH63078	Shrimp white spot
536	13.2	9.5	22	19	AAV21613	Human patched (ptc)	13.2	9.5	27	22	AAH62282	PME-VPLF PCR prime
537	13.2	9.5	22	19	AAV21613	Human patched (ptc)	13.2	9.5	27	22	AAH62282	Human genotyping p
538	13.2	9.5	22	22	AAH26383	Arabidopsis thalia	13.2	9.5	27	24	ABN88997	Human VPLF antibod
539	13.2	9.5	23	20	AAH76539	Human WISP-3 PCR p	13.2	9.5	27	24	ABN88997	Human VPLF antibod
540	13.2	9.5	23	24	ABL39565	Human cancer suppr	13.2	9.5	27	24	ABN88997	Human VPLF antibod
541	13.2	9.5	24	14	AAQ09233	Probe Polalpha #23	13.2	9.5	27	24	ABN88997	Human VPLF antibod
542	13.2	9.5	24	15	AAQ05800	Type II procollage	13.2	9.5	27	24	ABN88997	Human VPLF antibod
543	13.2	9.5	24	20	AAH57128	Human mutant KNO3	13.2	9.5	27	24	ABN88997	Human VPLF antibod
544	13.2	9.5	24	20	AAH57128	Human mutant KNO3	13.2	9.5	27	24	ABN88997	Human VPLF antibod
545	13.2	9.5	24	22	AAH16636	PCR primer for tel	13.2	9.5	27	24	ABN88997	Human VPLF antibod
546	13.2	9.5	24	22	AAH16636	Gastric acid produ	13.2	9.5	27	24	ABN88997	Human VPLF antibod
547	13.2	9.5	24	22	AAH16636	Human zinc finger	13.2	9.5	27	24	ABN88997	Human VPLF antibod
548	13.2	9.5	24	24	ABZ98398	Human hepsin/plasm	13.2	9.5	27	24	ABN88997	Human VPLF antibod
549	13.2	9.5	24	24	ABQ00667	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
550	13.2	9.5	24	24	ABQ03263	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
551	13.2	9.5	24	24	ABQ03317	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
552	13.2	9.5	24	24	ABQ05301	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
553	13.2	9.5	24	24	ABQ05342	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
554	13.2	9.5	24	24	ABQ11588	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
555	13.2	9.5	24	24	ABQ11588	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
556	13.2	9.5	24	24	AAH16174	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
557	13.2	9.5	25	19	AAV30645	HOMO DNA mismatch	13.2	9.5	27	24	ABN88997	Human VPLF antibod
558	13.2	9.5	25	22	AAH37671	Telomerase reverse	13.2	9.5	27	24	ABN88997	Human VPLF antibod
559	13.2	9.5	25	22	AAH37671	Human apoptosis li	13.2	9.5	27	24	ABN88997	Human VPLF antibod
560	13.2	9.5	25	22	AAH37671	SNP specific SNPE	13.2	9.5	27	24	ABN88997	Human VPLF antibod
561	13.2	9.5	25	24	ABV93312	SNP specific SNPE	13.2	9.5	27	24	ABN88997	Human VPLF antibod
562	13.2	9.5	25	24	ABV93313	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
563	13.2	9.5	25	24	ABV93314	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
564	13.2	9.5	25	24	ABV93315	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
565	13.2	9.5	25	24	ABV93316	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
566	13.2	9.5	25	24	ABV93317	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
567	13.2	9.5	25	24	ABV93318	Human POSHL1 scan	13.2	9.5	27	24	ABN88997	Human VPLF antibod
568	13.2	9.5	25	24	ABT03727	Human Otx-1 gene p	13.2	9.5	27	24	ABN88997	Human VPLF antibod
569	13.2	9.5	25	24	ABT03727	Oligonucleotide ad	13.2	9.5	27	24	ABN88997	Human VPLF antibod
570	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
571	13.2	9.5	25	24	ABN03465	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
572	13.2	9.5	25	24	ABN03466	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
573	13.2	9.5	25	24	ABN03467	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
574	13.2	9.5	25	24	ABN03469	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
575	13.2	9.5	25	24	ABN03470	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
576	13.2	9.5	25	24	ABN03471	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
577	13.2	9.5	25	24	ABN03472	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
578	13.2	9.5	25	24	ABN03472	Human GDMPLP-1 25-m	13.2	9.5	27	24	ABN88997	Human VPLF antibod
579	13.2	9.5	26	18	AAV12375	Toxicologically re	13.2	9.5	29	22	ABH43138	PCR primer OGR33 f
580	13.2	9.5	26	18	AAV12375	Primer (nt 1646-16	13.2	9.5	29	22	ABH43138	PCR primer OGR33 f
581	13.2	9.5	26	20	AAH89203	Hepatitis C virus	13.2	9.5	29	24	ABK96021	S. coelicolor accB
582	13.2	9.5	26	20	AAH89203	Human DRAX2 DNA cl	13.2	9.5	29	24	ABK96021	SELEX process nucl
583	13.2	9.5	26	21	AAZ60622	Probe meca360-26 f	13.2	9.5	29	24	ABK96021	SELEX process nucl
584	13.2	9.5	26	21	AAZ60622	PCR primer used to	13.2	9.5	29	24	ABK96021	Saccharomyces cere
585	13.2	9.5	26	21	AAZ65190	Primer amplifying	13.2	9.5	29	24	ABK96021	Vaccinia virus D4R
586	13.2	9.5	26	21	AAZ65190	Neisseria species	13.2	9.5	29	24	ABK96021	Vaccinia virus D4R
587	13.2	9.5	26	22	AAH83961	pCHEX vector seque	13.2	9.5	29	25	ABX17467	Ratt growth hormone
588	13.2	9.5	26	22	AAH83961	EAP28 gene fragmen	13.2	9.5	29	25	ABX17467	PCR primer used to
589	13.2	9.5	26	24	ABX97451	Human NOV-associat	13.2	9.5	30	20	AAH19510	Human lipocalin ho
590	13.2	9.5	26	24	ABX97451	Human gene specif	13.2	9.5	30	20	AAH19510	Human delta-2 prim
591	13.2	9.5	26	25	ABX80280	Human secreted or	13.2	9.5	30	21	AAH12531	Primer CRE4Rused t
592	13.2	9.5	26	25	ABX80280	Human secreted/tra	13.2	9.5	30	22	AAH12531	PCR primer for a p
593	13.2	9.5	26	25	ABX80280	Human secreted/tra	13.2	9.5	30	22	AAH12531	Barley nitrate red
594	13.2	9.5	26	25	ABX80280	Human secreted/tra	13.2	9.5	30	22	AAH12531	Mouse DSS-induced
595	13.2	9.5	26	25	ABX80280	Human secreted/tra	13.2	9.5	30	22	AAH12531	Mouse DSS-induced

812	13	9.4	30	24	ABK94875	Pat regulated gene
813	13	9.4	30	24	ABK94860	Degenerate PCR pri
814	13	9.4	30	24	ABA98688	Human SSA-56KDa PC
815	13	9.4	30	25	ABZ70455	Mouse TREM-1 forwa
816	12.8	9.2	17	16	AAQ91452	Dysprosium (III) t
817	12.8	9.2	17	18	AAZ75159	Mouse flt-1 VEGF r
818	12.8	9.2	17	19	AAV07298	Metallotexaphyrin-
819	12.8	9.2	17	20	AAV93414	Human B-raf subatr
820	12.8	9.2	17	20	AAV93413	Human B-raf subatr
821	12.8	9.2	17	20	AAV91007	Human C-raf target
822	12.8	9.2	17	21	AAZ79844	Hepatitis B virus
823	12.8	9.2	17	24	ABK97987	Human urokinase ge
824	12.8	9.2	17	24	ABK17683	Human ERG hamerthe
825	12.8	9.2	17	24	ABK18660	Human ERG G-cleave
826	12.8	9.2	17	24	ABL31561	Human HLA genotypi
827	12.8	9.2	18	16	AAQ91453	Dysprosium (III) t
828	12.8	9.2	18	19	AAV07301	Metallotexaphyrin-
829	12.8	9.2	18	21	AAZ92609	Antisense oligonuc
830	12.8	9.2	18	21	AAZ92642	Antisense oligonuc
831	12.8	9.2	19	18	AAV01272	Chymotrypsinogen P
832	12.8	9.2	19	19	AAV34507	BRCA1 exon 21 reve
833	12.8	9.2	19	21	AAZ82742	cdk3 ribozyme bind
834	12.8	9.2	19	21	AAZ82742	Raf-1 PCR primer
835	12.8	9.2	19	21	AAZ82742	Cell-cycle depende
836	12.8	9.2	19	22	AAH57904	Dysprosium (III) t
837	12.8	9.2	20	16	AAQ08086	Metallotexaphyrin-
838	12.8	9.2	20	20	AAZ95185	PCR primer used to
839	12.8	9.2	20	20	AAZ72568	Human biallelic ma
840	12.8	9.2	20	22	AAH80477	Oligonucleotide hy
841	12.8	9.2	20	22	AAH80477	Oligonucleotide hy
842	12.8	9.2	20	22	AAH80479	Oligonucleotide hy
843	12.8	9.2	20	22	AAH80480	Oligonucleotide hy
844	12.8	9.2	20	22	AAH80481	Oligonucleotide hy
845	12.8	9.2	20	22	AAC63224	HIV-KT PCR primer
846	12.8	9.2	20	23	ABZ72122	Gene 216 SSCP dete
847	12.8	9.2	20	23	ABZ72122	TNFR1 expression m
848	12.8	9.2	20	24	ABT50182	Human hepatocellul
849	12.8	9.2	20	24	ABK70680	Human hepatocellul
850	12.8	9.2	20	24	ABK70698	TRAK detection pr
851	12.8	9.2	20	24	AAI72572	Murine SAC1 gene-s
852	12.8	9.2	20	24	AAZ97795	Human TRAK-2 cDNA
853	12.8	9.2	20	24	AAZ97795	Human chromosome 1
854	12.8	9.2	20	24	AAZ97795	Human COPD related
855	12.8	9.2	20	25	ACC46833	Human gene 216 pol
856	12.8	9.2	20	25	ABX74975	Human gene 216 pol
857	12.8	9.2	20	25	ABX75035	Mouse ank gene PCR
858	12.8	9.2	20	25	ABZ22323	Human gene single
859	12.8	9.2	20	25	ABZ22323	Human polymorphic
860	12.8	9.2	21	23	AAH95385	Mouse B1 repetitiv
861	12.8	9.2	21	23	AAH95385	Human mutant KCNQ2
862	12.8	9.2	22	18	AAH95385	Sense PCR primer u
863	12.8	9.2	22	20	AAZ74265	Plant vector PCR p
864	12.8	9.2	22	20	AAZ74265	Myoplasma protect
865	12.8	9.2	22	20	AAZ74265	HIV-1 long termina
866	12.8	9.2	22	20	AAZ74265	CSF clones A14 B9
867	12.8	9.2	22	20	AAZ74265	Cytochrome c oxida
868	12.8	9.2	22	20	AAZ74265	PCR primer for the
869	12.8	9.2	22	20	AAZ74265	HG694A-24 primer
870	12.8	9.2	22	20	AAZ74265	Tyrosine phosphata
871	12.8	9.2	22	20	AAZ74265	HIV-1 long termina
872	12.8	9.2	22	20	AAZ74265	Human PRO1281 hybr
873	12.8	9.2	22	20	AAZ74265	Forward primer use
874	12.8	9.2	22	20	AAZ74265	Human dysferlin PC
875	12.8	9.2	22	20	AAZ74265	Human Gysferlin PC
876	12.8	9.2	22	20	AAZ74265	PCR primer RFL1600
877	12.8	9.2	22	20	AAZ74265	Human P2Y4 recepto
878	12.8	9.2	22	20	AAZ74265	Rat pro-collagen t
879	12.8	9.2	22	20	AAZ74265	Human P2Y4 recepto
880	12.8	9.2	22	20	AAZ74265	Rat pro-collagen t
881	12.8	9.2	22	20	AAZ74265	Human P2Y4 recepto
882	12.8	9.2	22	20	AAZ74265	Human P2Y4 recepto
883	12.8	9.2	22	20	AAZ74265	Human P2Y4 recepto
884	12.8	9.2	22	20	AAZ74265	Nucleic acid detec
885	12.8	9.2	24	24	ABK85949	Human beta globin
886	12.8	9.2	24	24	ABK85949	Human retinoblasto
887	12.8	9.2	24	24	ABK85949	PAR-1B control oli
888	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
889	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
890	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
891	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
892	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
893	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
894	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
895	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
896	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
897	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
898	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
899	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
900	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
901	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
902	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
903	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
904	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
905	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
906	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
907	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
908	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
909	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
910	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
911	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
912	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
913	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
914	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
915	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
916	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
917	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
918	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
919	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
920	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
921	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
922	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
923	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
924	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
925	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
926	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
927	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
928	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
929	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
930	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
931	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
932	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
933	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
934	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
935	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
936	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
937	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
938	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
939	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
940	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
941	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
942	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
943	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
944	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
945	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
946	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
947	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
948	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
949	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
950	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
951	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
952	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
953	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
954	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
955	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
956	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
957	12.8	9.2	24	24	ABK85949	Oligonucleotide ad

958	12.8	9.2	26	19	AAV24435	Probe MTB030 for M
959	12.8	9.2	26	19	AAV12998	Mycobacterium tuberculosis
C 960	12.8	9.2	26	20	AAK27786	Sequence of juncti
C 961	12.8	9.2	26	22	AAFP90349	HIV-1 mRNA region
C 962	12.8	9.2	26	22	AAFP73345	Grand fir monoterp
963	12.8	9.2	26	22	AAFP73446	Grand fir monoterp
964	12.8	9.2	26	24	ABK66872	Human gene specif
C 965	12.8	9.2	26	25	ABZ81017	Human obesity poly
C 966	12.8	9.2	27	12	AQJ14055	Oligonucleotide an
C 967	12.8	9.2	27	14	AQJ43044	Cyn di primer (CDI
C 968	12.8	9.2	27	16	AQJ79607	Wild type HIV-1 TA
C 969	12.8	9.2	27	16	AAQ79610	HIV-1 TAR bulge su
C 970	12.8	9.2	27	18	AAAT65278	Oligonucleotide ta
C 971	12.8	9.2	27	18	AAAT65298	Oligonucleotide 10
C 972	12.8	9.2	27	19	AAV55440	C-mpl receptor ago
C 973	12.8	9.2	27	19	AAV20694	Primer 109-5' for
C 974	12.8	9.2	27	19	AAV20532	Oligonucleotide SE
C 975	12.8	9.2	27	19	AAV20594	T. aestivum Dga44
C 976	12.8	9.2	27	20	AAK05663	HIV-1 oligonucleot
C 977	12.8	9.2	27	21	AAZ30370	3' PCR primer used
C 978	12.8	9.2	27	22	AAH94218	Human inflammatory
C 979	12.8	9.2	27	22	AAH38375	SNP specific SNPE
C 980	12.8	9.2	27	22	AAAF81413	PCR primer GSPI fo
C 981	12.8	9.2	27	24	ABK87917	PCR primer, #2, us
C 982	12.8	9.2	27	24	AAK98423	Human v gene libra
C 983	12.8	9.2	27	24	ABA81957	HLA-A capture olig
C 984	12.8	9.2	27	24	ABA81962	HLA-A capture olig
C 985	12.8	9.2	27	24	ABA93250	Human NADH dehydro
C 986	12.8	9.2	27	25	ABZ79484	PCR primer for amp
C 987	12.8	9.2	27	25	ABZ74714	Human anti-rIMP-1
C 988	12.8	9.2	28	14	AAQ37827	Sequence of probe
C 989	12.8	9.2	28	16	AAQ84661	Fragment of human
C 990	12.8	9.2	28	17	AAAT15675	Reverse-Frame HGV
C 991	12.8	9.2	28	17	AAAT08872	Primer GE-9R for H
C 992	12.8	9.2	28	18	AAAT74667	pig myogenin gene
C 993	12.8	9.2	28	18	AAAT74670	pig myogenin gene
C 994	12.8	9.2	28	19	AAV66131	PCR primer GE-9R u
C 995	12.8	9.2	28	19	AAV56090	HGV primer GE-9R D
996	12.8	9.2	28	19	AAV29487	Primer used to scr
C 997	12.8	9.2	28	20	AAK16410	PCR primer used to
C 998	12.8	9.2	28	20	AAK02365	UCR primer used to
C 999	12.8	9.2	28	20	AAK23153	US5856134 seq ID 4
C1000	12.8	9.2	28	20	AAV927163	Hepatitis G virus
						Reverse PCR primer

Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;
Matsuzawa Y;
WPI; 2001-611516/70.
Determining a risk factor for arteriosclerosis comprises detecting
mutations in genes for cholesterol ester transfer protein. -
Disclosure; Page 21; 58pp; Japanese.
The invention relates to detecting the risk factor for arteriosclerosis
in a subject that involves detecting mutations in the gene for
cholesterol ester transfer protein (CETP) related to the degree of risk
of arteriosclerosis. The mutant proteins alter the level of HDL in the
blood. The high frequency mutations can be detected for prevention and
treatment of arteriosclerosis. Sequences AA16655-91 represent PCR
primers related to the human CETP DNA, used during the course of the
invention.

Sequence 21 BP: 5' A...G C...G G...A T...A other...

CC N-acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
 CC (GPI-1) gene that is associated with low serum high density lipoprotein
 CC (HDL). The methods of the invention are useful for detecting a
 CC predisposition to high serum cholesterol, low serum HDL and
 CC cardiovascular disease. The methods are also useful for elucidating
 CC pathological pathways, developing diagnostic assays and new drug
 CC therapies for such disorders. The present DNA sequence represents a PCR
 CC primer used to amplify a human gene that is associated with high serum
 CC cholesterol, low serum HDL and/or cardiovascular disease.
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 14.4%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTGTAGCAGAGGCGAACA 28
 |||||
 DB 20 CTTGTAGCAGAGGCGAACA 1

RESULT 3

ABX12175/c

ID ABX12175 standard; DNA; 20 BP.

XX
 AC ABX12175;

DT 16-MAY-2003 (first entry)

XX Human cholesteryl ester transfer protein, reverse PCR primer.
 XX

XX Human; cholesteryl ester transfer protein; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
 KW antiseize; PCR; primer; ss.
 XX

XX Homo sapiens.
 XX

XX WO2003014306-A2.
 XX

XX 20-FEB-2003.
 XX

XX 05-AUG-2002; 2002WO-US24919.
 XX

XX 08-AUG-2001; 2001US-0925139.
 XX

XX (ISIS-) ISIS PHARM INC.
 XX

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
 PI WPI; 2003-248014/25.
 XX

XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease -
 XX

PS Example 13; Page 93; 114pp; English.
 XX

XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, PCR primer.
 XX

SQ Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 other;

Query Match

Best Local Similarity 14.4%; Score 20; DB 25; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 CGTGTGGAAGCTTGGTTAG 84
 |||||

DB 20 CGTGTGGAAGCTTGGTTAG 1

RESULT 4

ABX12198/c

ID ABX12198 standard; DNA; 20 BP.

XX
 AC ABX12198;

DT 16-MAY-2003 (first entry)

XX Human cholesteryl ester transfer protein, antisense oligo #19.
 XX

XX Human; cholesteryl ester transfer protein; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
 KW antiseize; probe; ss.
 XX

XX Homo sapiens.
 XX

XX Key Location/Qualifiers
 XX modified_base 1..6
 FT /mod_base= OTHER
 FT

FT modified_base 1..20
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT /mod_base= OTHER
 FT

FT modified_base 15..20
 FT /note= "Phosphorothioate nucleotides; all cytidine
 FT residues are 5-methylcytidines"
 FT

FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX

XX WO2003014306-A2.
 XX

XX 20-FEB-2003.
 XX

XX 05-AUG-2002; 2002WO-US24919.
 XX

XX 08-AUG-2001; 2001US-0925139.
 XX

XX (ISIS-) ISIS PHARM INC.
 XX

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
 PI WPI; 2003-248014/25.
 XX

XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease -
 XX

PS Claim 3; Page 96; 114pp; English.
 XX

XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, antisense
 CC oligonucleotide of the invention.
 XX

SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match

Best Local Similarity 14.4%; Score 20; DB 25; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGGGCTTGTAGCAGAA 20
 |||||

DB 20 GGATGGGCTTGTAGCAGAA 1
 |||||

RESULT 5

ABX12199/c

ID ABX12199 standard; DNA; 20 BP.
XX AC ABX12199;
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #20.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PP 05-AUG-2002; 2002WO-US24919.
XX PR 08-AUG-2001; 2001US-0925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX WPI; 2003-248014/25.
XX DR New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridizes with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 CTGGAACCCCTGGTGTCTCT 60
Db 20 CTGGAACCCCTGGTGTCTCT 1
RESULT 6
ID ABX12200/c
XX AC ABX12200 standard; DNA; 20 BP.
XX AC ABX12200;
XX DT 16-MAY-2003 (first entry)

XX DE Human cholesteryl ester transfer protein, antisense oligo #21.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PP 05-AUG-2002; 2002WO-US24919.
XX PR 08-AUG-2001; 2001US-0925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX WPI; 2003-248014/25.
XX DR New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridizes with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 GGAAGTTGGTTAGGAGTAC 90
Db 20 GGAAGTTGGTTAGGAGTAC 1
RESULT 7
ID ABX12217/c
XX AC ABX12217 standard; DNA; 20 BP.
XX AC ABX12217;
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #38.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;

antisense; probe; ss.
KW XX OS Homo sapiens.
XX XX
FH FT Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN PN WO2003014306-A2.
XX XX
XX XX 20-FEB-2003.
XX XX
XX XX 05-AUG-2002; 2002WO-US24919.
XX XX
XX XX 08-AUG-2001; 2001US-0925139.
XX XX (ISIS-) ISIS PHARM INC.
XX XX
XX XX Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX WPI; 2003-248014/25.
XX
XX New antisense compound, useful for preparing a composition for treating
FT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridizes with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GCTTGTAGCAGGACGAC 27
DB 20 GCTTGTAGCAGGACGAC 1
RESULT 8
ABX12218/c
ID ABX12218 standard; DNA; 20 BP.
XX XX
AC ABX12218;
XX XX
DT 16-MAY-2003 (first entry)
XX XX
DE Human cholesteryl ester transfer protein, antisense oligo #39.
XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER

modified_base 1..6
/mod_base= OTHER
modified_base 1..20
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
modified_base 15..20
/mod_base= OTHER
/note= "Phosphorothioate nucleotides; all cytidine
residues are 5-methylcytidines"
modified_base 15..20
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
WO2003014306-A2.
20-FEB-2003.
05-AUG-2002; 2002WO-US24919.
08-AUG-2001; 2001US-0925139.
(ISIS-) ISIS PHARM INC.
Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
WPI; 2003-248014/25.
New antisense compound, useful for preparing a composition for treating
abnormal lipid or cholesterol metabolism, atherosclerosis or
cardiovascular disease
Claim 3; Page 97; 114pp; English.
The invention relates to new antisense compounds targeted to a nucleic
acid molecule encoding human cholesteryl ester transfer protein,
specifically hybridizes with it and inhibits the expression of human
cholesteryl ester transfer protein. The compound is useful for preparing
a composition for treating abnormal lipid or cholesterol metabolism,
atherosclerosis or cardiovascular disease. The present sequence
represents a human cholesteryl ester transfer protein, antisense
oligonucleotide of the invention.
Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 63 AGCGTGTGGAGTTGGTT 82
DB 20 AGCGTGTGGAGTTGGTT 1
RESULT 9
ABX12219/c
ID ABX12219 standard; DNA; 20 BP.
XX XX
AC ABX12219;
XX XX
DT 16-MAY-2003 (first entry)
XX XX
DE Human cholesteryl ester transfer protein, antisense oligo #40.
XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER

```
FT /note= "Phosphorothioate nucleotides; all cytidine
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003014306-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US24919.
XX
XX 08-AUG-2001; 2001US-0925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-248014/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridises with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 other;
SQ
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 84 GGAGTACCGAGATGGAGATT 103
Db 20 GGAGTACCGAGATGGAGATT 1
RESULT 10
ABX12220/c
ID ABX12220 standard; DNA; 20 BP.
XX
XX AC ABX12220;
XX
XX 16-MAY-2003 (first entry)
XX
XX Human cholesteryl ester transfer protein, antisense oligo #41.
XX
XX Human; cholesteryl ester transfer protein; lipid metabolism;
XX cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX /mod_base= OTHER
XX
XX modified_base 1..20
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX modified_base 15..20
XX /note= "Phosphorothioate nucleotides; all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 15..20
XX /mod_base= OTHER
XX
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
```

```
XX WO2003014306-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US24919.
XX
XX 08-AUG-2001; 2001US-0925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-248014/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridises with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 other;
SQ
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 120 CTATCTTAAGGCCCACTGG 139
Db 20 CTATCTTAAGGCCCACTGG 1
RESULT 11
AAT50642
ID AAT50642 standard; RNA; 18 BP.
XX
XX AC AAT50642;
XX
XX 10-MAR-1997 (first entry)
XX
XX Human CETP hairpin ribozyme target sequence #1669.
XX
XX Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypolipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX Homo sapiens.
XX
XX WO9620279-A1.
XX
XX 04-JUL-1996.
XX
XX 11-DEC-1995; 95WO-US16000.
XX
XX 23-DEC-1994; 94US-0363240.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Bisgaier C, Couture L, McSwiggen J, Page M, Stinchcomb D;
```

XX DR WPI; 1996-321852/32.

XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA

XX FT - useful for preventing or treating initial development, progression

XX PT or regression of vascular diseases, esp. familial

XX PT hypercholesterolaemia

XX CC Claim 4; Page 54; 72pp; English.

XX CC AAT50595-T50642 represent target sequences for the human cholesterol

XX CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).

XX CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer

XX CC between plasma lipoproteins. The numbering of the targets refers to the

XX CC position of the cleavage site in full length CETP. The ribozyme then

XX CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The

XX CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby

XX CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,

XX CC the reverse cholesterol transport (RCT) pathway can be inhibited (or

XX CC eliminated) thereby preventing the reduction in size density of the high

XX CC density lipoproteins (HDL), prolonging HDL half life, and therefore

XX CC increasing HDL levels. The ribozymes can be used to treat conditions

XX CC associated with abnormal levels of CETP, specifically atherosclerosis,

XX CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,

XX CC familial hypercholesterolaemia, hypobetalipoproteinaemia, vascular

XX CC complications of diabetes, transplant, atherectomy and angioplasty

XX CC restenosis. By inhibiting CETP, the levels of HDL and low density

XX CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a

XX CC decrease in LDL levels, and a corresponding increase in HDL levels). The

XX CC ribozymes can also be used diagnostically to study genetic drift and

XX CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes

XX CC target specific regions of the CETP gene, they have low non-specific

XX CC activity.

XX SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 U; 0 other;

Query Match 12.9%; Score 18; DB 17; Length 18;

Best Local Similarity 83.3%; Pred. No. 1.9e+04;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCTCACAGCTGGACCT 50

DB 1 GCUCACAGCUGGACCCU 18

RESULT 12

AA37644

ID AAX37644 standard; DNA; 22 BP.

AC AAX37644;

DT 08-JUL-1999 (first entry)

XX HBV detecting primer 8.

XX Detection; HBV; real time; PCR; reporter; fluorescent; primer;

XX quencher; fluorescence resonance energy transfer; ss.

XX Synthetic.

XX Hepatitis B virus.

XX JP11103897-A.

XX 20-APR-1999.

XX 30-SEP-1997; 97JP-0282612.

XX 30-SEP-1997; 97JP-0282612.

XX (SRLS-) SRL KK.

XX WPI; 1999-305860/26.

XX

PT New primers and probes - for measurement of an Herpes B Virus (HBV)

PT gene by a real time detecting PCR

XX Example 2; Page 8; 12pp; Japanese.

XX This invention describes a method for the measurement of an HBV gene by

XX a real time detecting PCR. The invention also describes a method for the

XX measurement of an HBV gene by a real time detecting PCR in which a

XX reporter fluorescent colour and a quencher fluorescent colour are

XX combined to an oligonucleotide, the fluorescence of said reporter

XX fluorescent colour is controlled by fluorescence resonance energy

XX transfer when reporter fluorescent colour is combined to the same probe

XX as quencher fluorescent colour. The method can measure an HBV exactly in

XX a high sensitivity.

XX SQ Sequence 22 BP; 5 A; 11 C; 1 G; 5 T; 0 other;

Query Match 12.4%; Score 17.2; DB 20; Length 22;

Best Local Similarity 86.4%; Pred. No. 3.6e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 108 CCCAACTCCTCCCTATCCTAAA 129

DB 1 CCCAACTCCTCCAGTCCTTAA 22

RESULT 13

AA37644

ID AAX22550 standard; mRNA; 17 BP.

XX AAX22550;

XX 21-MAY-1999 (first entry)

XX Human CETP RNA fragment #5.

XX CETP; cholesterol ester transfer protein; inhibitor; therapy; treatment;

XX surface plasmon resonance; vascular disease; pathogenic; atherosclerosis;

XX human; ss.

XX Homo sapiens.

XX DE19731609-A1.

XX 18-FEB-1999.

XX 23-JUL-1997; 97DE-1031609.

XX 23-JUL-1997; 97DE-1031609.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX Budzinski R, Krist B, Mark M, Mueller P;

XX WPI; 1999-143775/13.

XX RNA transcript of human cholesteryl ester transfer protein gene -

XX useful in drug screening assays, especially for atherosclerosis

XX Disclosure; Page 13; 24pp; German.

XX This invention describes the isolation of a transcript of the human

XX cholesteryl ester transfer protein (CETP) gene having a 5' untranslated

XX region including a regulatory sequence. The invention also describes

XX a method (a) for identifying substances capable of inhibiting CETP gene

XX expression, comprising measuring the translation rate of the above

XX transcript in the presence of a test substance, (2) a test substance

XX capable of inhibiting CETP gene expression, (3) an antisense

XX oligonucleotide capable of binding to the 5' untranslated region of the

XX above transcript and (4) a method based on surface plasmon resonance for

XX measuring the binding of a substance to a nucleic acid. The test

XX substance of (2) and the oligonucleotide of (3) are useful for

XX prophylactic or therapeutic treatment of vascular diseases in which CETP

CC has a pathogenic role, especially atherosclerosis.
 XX Sequence 17 BP; 2 A; 8 C; 1 G; 6 U; 0 other;
 SQ Query Match 12.2%; Score 17; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GAGTACGAGATGGAGA 101
 DB 17 GAGTACGAGATGGAGA 1

RESULT 14
 AAI99829
 ID AAI99829 standard; DNA; 21 BP.
 AC AAI99829;
 XX 28-JAN-2002 (first entry)
 DT Human G protein-coupled receptor protein TGR5 PCR primer SEQ ID NO 5.
 DE Human; TGR5; G protein-coupled receptor protein; cerebroprotective;
 KW human; immunomodulator; cytosolic; antiinflammatory; antidiabetic;
 KW cancer; PCR primer; ss.
 XX Homo sapiens.
 OS WO200177325-A1.
 FN 18-OCT-2001.
 PD 12-APR-2001; 2001WO-JP03143.
 PF 12-APR-2000; 2000JP-0110765.
 PR (TAKE) TAKEDA CHEM IND LTD.
 PA Miwa M, Matsui H, Shintani Y;
 PI WPI; 2002-010910/01.
 DR Human brain-originated G protein-coupled receptor protein TGR5,
 XX applicable in diagnosis and developing drugs for diseases of e.g.
 PT central nervous system and digestive organs, inflammation, cancer and
 PT diabetes -
 XX Example 2; Page 98; 104pp; Japanese.
 PS The invention relates to a novel human G protein-coupled receptor protein
 CC TGR5 and the encoding cDNA with cerebroprotective, cardiant,
 CC immunomodulator, cytosolic, antiinflammatory and antidiabetic activity.
 CC The protein, encoded DNA and anti-TGR5 antibody are applicable in
 CC diagnosis and developing drugs for diseases of central nervous system and
 CC circulatory organs, inflammation, cancer and diabetes. The present
 CC sequence is that of a TGR5 PCR primer of the invention.
 XX Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
 SQ Query Match 12.1%; Score 16.8; DB 24; Length 21;
 Best Local Similarity 90.0%; Pred. No. 4.8e+04;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 102 TTGGCTCCCAACTCTCCCT 121
 DB 1 TTGGCTCCCAACTCTCTCTT 20

RESULT 15
 AAX21403
 ID AAX21403 standard; DNA; 27 BP.
 XX

AC AAX21403;
 XX 21-MAY-1999 (first entry)
 DT T.ni acyl-CoA delta-11-desaturase primer 5'-delta-9dl.
 DE Membrane; acyl-CoA delta-11 desaturase; pheromone gland; moth; primer;
 XX fatty acyl-CoA reactant; attraction; insect; trap; PCR; ss.
 KW Synthetic.
 OS Trichoplusia ni.
 XX US5876994-A.
 FN 02-MAR-1999.
 PD 16-NOV-1995; 95US-0558823.
 PF 16-NOV-1995; 95US-0558823.
 PR (CORR) CORNELL RES FOUND INC.
 XX Knipple DC, Miller SJ, Roelofs WL;
 PI WPI; 1999-189641/16.
 DR New isolated acyl-CoA desaturase - obtained from the pheromone
 PT glands of insects, used for the production of unsaturated fatty
 PT acyl-CoA products which can be used for pheromone production
 XX Example 4; Column 22; 37pp; English.
 PS Primers AAX21402-X21403 were used to PCR amplify a fragment of the
 CC coding region of the membrane-associated acyl-CoA delta-11 desaturase
 CC (AAX21401) expressed in the pheromone gland of the moth Trichoplusia ni.
 CC The coding sequence (AAX21400) encodes a protein which contains the
 CC generic motifs: His-Xaa(4)-His, His-Xaa(2)-His-His or
 CC His-Xaa(4)-His-Xaa(30)-His-Xaa(2)-His-His-Xaa(135)-His-Xaa(2)-His-His.
 CC The desaturase can be used to produce a pheromone precursor by converting
 CC a saturated or unsaturated fatty acyl-CoA reactant to an unsaturated
 CC fatty acyl-CoA product which contains at least one more carbon-carbon
 CC double bond than the fatty acyl-CoA reactant. The mono-, di-, or
 CC poly-unsaturated fatty acid products obtained are useful as intermediates
 CC for the synthesis of diverse compounds that can be used as pheromones to
 CC attract particular species of insects, especially to a trap, where they
 CC can be restrained or killed.
 XX Sequence 27 BP; 4 A; 4 C; 4 G; 7 T; 8 other;
 SQ Query Match 12.1%; Score 16.8; DB 20; Length 27;
 Best Local Similarity 57.7%; Pred. No. 5.1e+04;
 Matches 15; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 58 CCTCCAGCGTGTGGAGTGGGTTA 83
 DB 2 CCTTCAGTGTGTGWTATGTGWA 27

RESULT 16
 AAS14772
 ID AAS14772 standard; CDNA; 30 BP.
 XX AAS14772;
 AC 29-JAN-2002 (first entry)
 DT Chicken II gonadotropin-releasing hormone (GnRH) analogue cDNA.
 DE GnRH; gonadotropin-releasing hormone; extra-pituitary GnRH receptor; ss;
 KW antitumour; cytostatic; mammal; post-proline peptidase; endopeptidase;
 KW blood; cell proliferation; metastasis; apoptosis; tumour regression;
 KW proliferative disorder; chicken; chicken II GnRH analogue; cancer;
 KW protein degradation.

XX OS Gallus gallus.
 XX FH Key
 XX CDS Location/Qualifiers
 XX 1..30
 XX /*tag= a
 XX /product= "Chicken II GnRH analogue peptide"
 XX /transl_except= (pos:1..3, aa:Glu)
 XX /transl_except= (pos:16..18, aa:Arg)
 XX /partial
 XX /note= "No start or stop codon"
 XX
 XX WO200174377-A1.
 XX
 XX 11-OCT-2001.
 XX
 XX 26-SEP-2000; 2000WO-US26575.
 XX
 XX 31-MAR-2000; 2000US-0540685.
 XX
 XX (KHOD/) SILER-KHODR T M.
 XX (KHOD/) KHODR G S.
 XX
 XX Siler-Khodr TM, Khodr GS;
 XX
 XX WPI; 2001-662948/76.
 XX P-PSDB; AAU08771.
 XX
 XX Non-mammalian gonadotropin-releasing hormone analogue capable of binding
 XX to hormone receptors in tumour cell with greater affinity and resistant
 XX to degradation by tumour tissue enzymes, useful in tumour growth
 XX regulation
 XX
 XX Claim 12; Page 39; 49pp; English.
 XX
 XX The invention relates to a composition comprising a non-mammalian
 XX gonadotropin-releasing hormone (GnRH) analogue for regulating tumour GnRH
 XX activity, where the analogue is capable of binding to extra-pituitary
 XX GnRH receptors expressed on tumour tissues. The analogue has a greater
 XX binding affinity than mammalian GnRH and is resistant to degradation by
 XX post-proline peptidases, particularly those found around tumour tissues,
 XX and endopeptidases found circulating in the blood. GnRH analogues are
 XX useful for regulating tumour activity by acting as superagonists at
 XX tumour tissue, leading to tissue receptor down regulation. The peptides
 XX act to reduce tumour cell proliferation and metastasis and can induce
 XX apoptosis and tumour regression. GnRH analogues are also useful for
 XX producing antibodies that specifically bind to non-mammalian GnRH peptide
 XX sequences or to tumour tissues or any other non-pituitary GnRH peptide or
 XX protein, for the treatment of proliferative disorders. This sequence
 XX represents cDNA encoding a chicken II GnRH analogue peptide.
 XX
 XX SQ Sequence 30 BP; 5 A; 8 C; 9 G; 8 T; 0 other;
 XX
 XX Query Match 12.1%; Score 16.8; DB 22; Length 30;
 XX Best Local Similarity 75.0%; Pred. No. 5.3e+04;
 XX Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 XX
 XX QY 25 AGCACCAGGCTCACAGCTGGAACCTGG 52
 XX ||||| ||||| ||||| ||||| |||||
 XX Db 2 AGCACTGGTCTCATGGCTGTATCTCTGG 29
 XX
 XX RESULT 17
 XX AAD44973
 XX ID AAD44973 standard; cDNA; 30 BP.
 XX
 XX AC AAD44973;
 XX
 XX DT 27-DEC-2002 (first entry)
 XX
 XX DE Chicken gonadotropin releasing hormone (GnRH) cDNA.
 XX
 XX XX Chicken; gonadotropin releasing hormone; postcoital contraceptive agent;

KW GnRH; pregnancy; ovarian cyst; endometriosis; polycystic ovarian disease;
 KW leiomyomas; luteolytic agent; fertility regulation; menses-inducing agent;
 KW abnormal uterine bleeding; abnormal pregnancy; trophoblastic disease;
 KW ectopic pregnancy; molar pregnancy; human chorionic gonadotropin; hCG;
 KW abortion; gynaecological; cytostatic; abortifacient; contraceptive; gene;
 KW ss.
 XX Gallus gallus.
 XX Key
 XX CDS Location/Qualifiers
 XX 1..30
 XX /*tag= a
 XX /product= "Chicken GnRH decapeptide"
 XX /transl_except= (pos:1..3, aa:p-Glu)
 XX /note= "This translational exception occurs when decoding
 XX the GnRH peptides shown as SEQ ID NO: 2 in claim 4, 1 and
 XX page 18 of the specification (AAE28135, AAE28137 and
 XX AAE28138 respectively)"
 XX /transl_except= (pos:16..18, aa:D-Arg)
 XX /note= "This translational exception occurs only when
 XX decoding the GnRH peptides shown as SEQ ID NO: 2 in
 XX claim 1 and page 18 of the specification (AAE28135 and
 XX AAE28138 respectively)"
 XX /transl_except= (pos:16..18, aa:Xaa)
 XX /note= "Xaa corresponds to D-Arg; This translational
 XX exception occurs only when decoding the GnRH peptide
 XX shown as SEQ ID NO: 2 in claim 1 of the specification
 XX (AAE28137)"
 XX /transl_except= (pos:28..30, aa:Xaa)
 XX /note= "Xaa corresponds to aza-Gly; This translational
 XX exception occurs only when decoding the GnRH peptides
 XX shown as SEQ ID NO: 2 in claim 4 and claim 1 of the
 XX specification (AAE28135 and AAE28137); CDS does not
 XX include start and stop codon"
 XX /partial
 XX
 XX US2002065226-A1.
 XX 30-MAY-2002.
 XX
 XX 28-AUG-2001; 2001US-0941094.
 XX
 XX 15-OCT-1999; 99US-0419161.
 XX (SILE/) SILER-KHODR T.
 XX
 XX Siler-Khodr T;
 XX
 XX WPI; 2002-681323/73.
 XX P-PSDB; AAE28135, AAE28137, AAE28138.
 XX
 XX Novel non-mammalian gonadotropin releasing hormone analogs useful to
 XX regulate reproductive functions and disorders, as menses regulators,
 XX contraceptives or abortifacients --
 XX
 XX Claim 15; Page 19; 57pp; English.
 XX
 XX The present invention relates to novel non-mammalian peptide hormone
 XX analogues of gonadotropin releasing hormone (GnRH) capable of binding
 XX to ovarian, tubal, endometrial, uterine, prostate or testicular GnRH
 XX receptors and active in the presence of a post-proline peptidase or an
 XX endopeptidase. Sequences of the invention are useful for regulating and
 XX treating a condition of the ovaries, fallopian tubes, uterus, prostate,
 XX endometrium, testicles or tissues of pregnancy in a patient or animal.
 XX They are useful in various treatment methods as a contraceptive or post-
 XX coital contraceptive agent, for maintaining pregnancy when used in very
 XX low doses and administered in pulsatile fashion. GnRH analogues of the
 XX invention are useful in the preparations for the treatment of ovarian
 XX cysts, endometriosis and leiomyomas. They are useful as luteolytic agents,
 XX in fertility regulation, as menses-inducing agents and the management of
 XX ovarian cyst, polycystic ovarian disease, abnormal uterine bleeding, in
 XX vitro fertilisation protocols, abnormal pregnancies, ectopic pregnancies,
 XX molar pregnancies and trophoblastic disease. Sequences of the invention

hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.

Sequence 29 BP; 3 A; 8 C; 5 G; 12 T; 1 other;

Query Match 11.8%; Score 16.4; DB 21; Length 29;

Best Local Similarity 71.4%; Pred. No. 7.1e+04;

Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 11 TGTAGCAGAGGCAAGCAACAGGCTCAC 38

DB 28 TGAAGAAGAGGCTGACACGACTTAC 1

RESULT 20

ACC46916/c

ID ACC46916 standard; DNA, 30 BP.

AC ACC46916;

XX

DT 05-JUN-2003 (first entry)

XX

DE Mouse phospholipase A2 group IIA probe SEQ ID NO:13.

XX

KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetes; probe; ss.

XX

OS Mus musculus.

OS Synthetic.

XX

PN WO200297133-A1.

XX

PD 05-DEC-2002.

XX

PF 21-MAY-2002; 2002WO-US16135.

XX

PR 25-MAY-2001; 2001US-0865866.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Wyatt JR;

XX

DR WPI; 2003-140495/13.

XX

PT New compound that hybridizes with and inhibits the expression of

PT Phospholipase A2, group IIA, useful for preparing a composition for

PT treating or preventing inflammation, cancer, psoriasis or diabetes

PS

Example 13; Page 84; 135pp; English.

XX

CC The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 3' UTR or intron region of a nucleic acid molecule encoding phospholipase A2, group IIA (synovial), where the compound specifically hybridizes with and inhibits the expression of phospholipase A2, group IIA (synovial).

CC Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, group IIA (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and antipsoriatic activities, and can be used in vaccines and in gene therapy. The compound (I) can be used for preparing a composition for

CC

CC

CC

CC

CC

CC treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a probe for mouse phospholipase A2 group IIA (synovial), which is used in an example from the present invention.

XX

SQ Sequence 30 BP; 4 A; 11 C; 3 G; 12 T; 0 other;

Query Match 11.8%; Score 16.4; DB 25; Length 30;

Best Local Similarity 76.9%; Pred. No. 7.1e+04;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 87 GTACGAGATGGAGATTGGCTCCAA 112

DB 28 GTACGAGAGGAGTGGATGCCAA 3

RESULT 21

AAV52705

ID AAV52705 standard; DNA; 22 BP.

XX

AC AAV52705;

XX

DT 21-DEC-1998 (first entry)

XX

DE Hepatocyte nuclear factor 1 beta gene exon 4-2 forward PCR primer.

XX

KW Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human;

KW transcription factor; maturity onset diabetes of the young; TCF2;

KW diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9811254-A1.

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PD 19-MAR-1998.

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PF 10-SEP-1997; 97WO-US16037.

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PR 30-OCT-1996; 96US-0029679.

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PR 10-SEP-1996; 96US-0025719.

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PR 02-OCT-1996; 96US-0028056.

XX

PA (ARCH-) ARCH DEV CORP.

XX

PI Bell GI, Furuta H, Horikawa Y, Kaisaki PJ, Menzel S;

XX

PI Oda N, Yamagata K;

XX

XX WPI; 1998-271667/24.

XX

PT Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young

XX

PS Example 8; Page 146; 363pp; English.

XX

CC This is a forward PCR primer designed for use with a reverse primer (see AAV52706) in the PCR amplification of the 4-2 exon of the human hepatocyte nuclear factor-1 beta (HNF-1 beta) TCF2 gene (see AAV52730). Mutations of the HNF-1 beta gene have been identified by amplifying (see AAV52693-716) and sequencing the appropriate exon. The invention concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It demonstrates that the MODY4 (maturity-onset diabetes of the young) locus is the HNF-1 beta gene. Analysis of mutations in the HNF-1 beta gene can be diagnostic for diabetes.

XX

SQ Sequence 22 BP; 8 A; 9 C; 3 G; 2 T; 0 other;

Query Match 11.7%; Score 16.2; DB 19; Length 22;

Best Local Similarity 85.7%; Pred. No. 7.7e+04;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 ACCAGGCTCAGCTGGAACC 48
 Db 2 ACCAGACTCAGAGCTGAACC 22

RESULT 22
 AAX56275/c
 ID AAX56275 standard; DNA; 28 BP.
 XX
 AC AAX56275;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Human neuronal apoptosis inhibiting protein PCR primer #2.
 XX
 KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
 KW spinal muscular atrophy; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN JP11116599-A.
 XX
 PD 27-APR-1999.
 XX
 PF 14-OCT-1997; 97JP-0280831.
 XX
 PR 14-OCT-1997; 97JP-0280831.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 1999-323531/27.
 XX
 PT New apoptosis inhibitory protein - useful for determining mechanism
 PT of various apoptotic diseases e.g. human spinal muscular atrophy
 XX
 PS Example 1; Page 15; 16pp; Japanese.
 XX
 CC The present sequence represents a PCR primer for human neuronal
 CC apoptosis inhibitory protein (NAIP). The apoptosis inhibitory protein
 CC is useful for the elucidation of the mechanism of various apoptosis
 CC diseases such as human spinal muscular atrophy and the diagnosis, the
 CC prevention and the treatment of such diseases.
 XX
 SQ Sequence 28 BP; 8 A; 8 C; 5 G; 7 T; 0 other;

Query Match 11.7%; Score 16.2; DB 20; Length 28;
 Best Local Similarity 85.7%; Pred. No. 8.1e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 62 CAGCGTGGTGAAGTTGGGTT 82
 Db 25 CAGCGTGGTGAAGTTGAATT 5

RESULT 23
 AAT60157/c
 ID AAT60157 standard; DNA; 30 BP.
 XX
 AC AAT60157;
 XX
 DT 01-DEC-1997 (first entry)
 XX
 DE Collagen gene promoter region binding oligomer Oligo Col TFOa.
 XX
 KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
 XX
 OS Synthetic.
 OS
 PN W09710254-A1.

XX 20-MAR-1997.
 XX
 PF 12-SEP-1996; 96WO-US14640.
 XX
 PR 11-SEP-1996; 96US-0712357.
 PR 15-SEP-1995; 95US-0528836.
 XX
 PA (GUNT/) GUNTAKA R V.
 XX
 PI Guntaka RV, Kandala J, Kovacs A, Weber KT;
 XX WPI; 1997-202172/18.
 XX
 DR Triplex forming oligomer binds to collagen gene promoter region -
 XX used to impede pathological fibrosis etc.
 XX
 PS Claim 18; Page 33; 52pp; English.
 XX
 CC An oligomer has been produced which is capable of inhibiting expression
 CC of a collagen gene. The present sequence represents a specifically
 CC claimed oligomer Oligo Col TFOa, which binds to the polypurine-
 CC polypyrimidine region of the rat alpha1(I) collagen gene promoter
 CC region. The oligomer may be used to impede pathological fibrosis which
 CC is associated with myocardial fibrosis in hypertensive heart diseases,
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin
 CC following burn injury. The oligomer inhibits expression of a collagen
 CC gene after insertion into a cell by causing an intracellular reaction
 CC which inhibits gene expression. The oligomer is preferably a triplex
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
 CC oligonucleotide corresponding to the noncoding strand of the promoter
 CC between -170 and -140. This section was chosen due to its binding
 CC stability at physiological pH.
 XX
 SQ Sequence 30 BP; 11 A; 0 C; 19 G; 0 U; 0 other;

Query Match 11.7%; Score 16.2; DB 18; Length 30;
 Best Local Similarity 85.7%; Pred. No. 8.3e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 106 CTCCTCAACTCTCCCTATCCT 126
 Db 30 CTCCTCCCTCTCTCTCTCTCT 10

RESULT 24
 AAZ98705/c
 ID AAZ98705 standard; DNA; 30 BP.
 XX
 AC AAZ98705;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Collagen promoter inhibitory oligonucleotide Oligo Col TFOa.
 XX
 KW Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
 KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
 KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
 XX
 OS Rattus sp.
 XX
 PN W0200008213-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US17824.
 XX
 PR 07-AUG-1998; 98US-0130888.
 XX
 PA (GUNT/) GUNTAKA R V.
 XX
 PI Guntaka RV, Weber KT, Kovacs A, Kandala J;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 10:09:59 ; Search time 47 Seconds
(without alignments)

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Title: US-09-925-139-3_COPY_1631_1769
Perfect score: 139
Sequence: 1 aaatgggggtttatgcacaa

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

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Minimum DB seq length: 0
Maximum DB seq length: 30
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Post-processing:	Minimum Match	0%
	Maximum Match	10%
	Listing first	10%

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	18	12.9	18	1	1	US-08-363-240A-1125	Sequence 1125, Ap
2	16.8	12.1	27	1	2	US-08-558-823-11	Sequence 11, Appl
3	16.8	12.1	30	4	3	US-09-419-161-1	Sequence 1, Appli
c 4	16.4	11.8	29	4	4	US-09-304-233-439	Sequence 439, App
5	16.2	11.7	22	3	5	US-08-927-219-102	Sequence 102, App
c 6	16.2	11.7	30	1	6	US-08-802-547-6	Sequence 6, Appli
c 7	16.2	11.7	30	1	7	US-08-712-357-6	Sequence 6, Appli
c 8	15.6	11.2	30	1	8	US-08-458-489-7	Sequence 7, Appli
c 9	15.6	11.2	30	1	9	US-08-458-686-7	Sequence 7, Appli
c 10	15.6	11.2	30	1	10	US-07-843-350C-7	Sequence 7, Appli
c 11	15.6	11.2	30	5	11	PGT-US93-01159-7	Sequence 7, Appli
12	15.2	10.9	23	3	12	US-09-161-466-19	Sequence 19, Appl
13	15.2	10.9	30	3	13	US-08-946-138-24	Sequence 24, Appl
14	15.2	10.9	30	3	14	US-09-130-546D-24	Sequence 24, Appl
15	15.2	10.9	30	4	15	US-09-227-694B-24	Sequence 24, Appl
16	15.2	10.9	30	4	16	US-09-446-081-26	Sequence 26, Appl
17	15	10.8	15	1	17	US-08-363-240A-240	Sequence 240, App
18	15	10.8	15	1	18	US-08-363-240A-241	Sequence 241, App
19	15	10.8	15	1	19	US-08-363-240A-241	Sequence 241, App
20	15	10.8	15	1	20	US-08-363-240A-242	Sequence 242, App
21	15	10.8	15	1	21	US-08-363-240A-243	Sequence 243, App
22	15	10.8	15	1	22	US-08-363-240A-244	Sequence 244, App
23	15	10.8	15	1	23	US-08-363-240A-245	Sequence 245, App
24	15	10.8	15	1	24	US-08-363-240A-246	Sequence 246, App
25	15	10.8	15	1	25	US-08-363-240A-247	Sequence 247, App
26	15	10.8	15	1	26	US-08-363-240A-248	Sequence 248, App
27	15	10.8	15	1	27	US-08-363-240A-249	Sequence 249, App
	15	10.8	15	1		US-08-363-240A-250	Sequence 250, App

101	14.2	10.2	30	4	US-09-119-507B-53	Sequence 53, Appl	174	13.4	9.6	24	1	US-07-977-284A-73	Sequence 73, Appl
102	14.2	10.2	30	4	US-09-119-507B-110	Sequence 110, Appl	175	13.4	9.6	24	2	US-08-256-426B-73	Sequence 73, Appl
C 103	14.2	10.2	30	4	US-08-897-556A-11	Sequence 11, Appl	C 176	13.4	9.6	25	2	US-08-500-914A-4	Sequence 4, Appl
104	14.2	10.2	30	4	US-08-897-556A-53	Sequence 53, Appl	C 177	13.4	9.6	25	2	US-08-859-998-554	Sequence 554, Appl
C 105	14	10.1	22	4	US-08-301-533-98	Sequence 98, Appl	C 178	13.4	9.6	27	3	US-08-513-974B-2	Sequence 2, Appl
106	14	10.1	24	1	US-08-324-301-21	Sequence 21, Appl	C 179	13.4	9.6	27	3	US-08-513-974B-76	Sequence 76, Appl
C 107	14	10.1	24	1	US-08-324-301-22	Sequence 22, Appl	C 180	13.4	9.6	27	3	US-08-776-971-30	Sequence 30, Appl
C 108	14	10.1	25	2	US-08-828-008-8	Sequence 8, Appl	C 181	13.4	9.6	27	4	US-09-225-928-554	Sequence 554, Appl
C 109	14	10.1	25	4	US-09-402-631A-15	Sequence 15, Appl	C 182	13.4	9.6	27	4	US-08-540-050B-8	Sequence 26, Appl
110	14	10.1	25	4	US-09-645-629-11	Sequence 11, Appl	C 183	13.4	9.6	27	4	US-08-793-273C-26	Sequence 554, Appl
111	14	10.1	29	4	US-09-304-232-693	Sequence 693, Appl	C 184	13.4	9.6	27	4	US-09-225-201B-554	Sequence 6, Appl
112	14	10.1	30	2	US-08-250-346-26	Sequence 26, Appl	C 185	13.4	9.6	27	4	US-09-255-518C-6	Sequence 63, Appl
C 113	13.8	9.9	20	4	US-09-844-525A-74	Sequence 74, Appl	C 186	13.4	9.6	27	4	US-08-403-459-63	Sequence 2, Appl
114	13.8	9.9	20	4	US-08-921-497-4	Sequence 4, Appl	C 187	13.4	9.6	27	4	US-09-461-438B-2	Sequence 2, Appl
115	13.8	9.9	26	1	US-08-388-779A-11	Sequence 11, Appl	C 188	13.4	9.6	29	4	US-09-304-232-345	Sequence 345, Appl
116	13.8	9.9	26	1	US-08-591-070A-11	Sequence 11, Appl	C 189	13.4	9.6	29	4	US-08-678-039A-13	Sequence 13, Appl
117	13.8	9.9	26	2	US-08-927-855-11	Sequence 11, Appl	C 190	13.4	9.6	30	2	US-09-170-496D-115	Sequence 115, Appl
118	13.8	9.9	27	1	US-07-825-959-13	Sequence 13, Appl	C 191	13.4	9.6	30	4	US-08-802-547-12	Sequence 12, Appl
C 119	13.8	9.9	27	1	US-08-131-324-13	Sequence 13, Appl	C 192	13.2	9.5	18	1	US-08-712-357-12	Sequence 12, Appl
C 120	13.8	9.9	27	3	US-08-325-426B-10	Sequence 10, Appl	C 193	13.2	9.5	18	3	US-09-255-912-28	Sequence 28, Appl
C 121	13.8	9.9	29	1	US-08-683-877-12	Sequence 12, Appl	C 194	13.2	9.5	18	3	US-09-280-409-75	Sequence 75, Appl
122	13.8	9.9	30	1	US-08-105-483-455	Sequence 455, Appl	C 195	13.2	9.5	18	3	US-09-721-534-10	Sequence 10, Appl
123	13.8	9.9	30	1	US-08-703-209-455	Sequence 455, Appl	C 196	13.2	9.5	18	3	US-09-723-534-10	Sequence 10, Appl
124	13.8	9.9	30	1	US-08-303-275-167	Sequence 167, Appl	C 197	13.2	9.5	18	4	US-09-077-619-15	Sequence 15, Appl
C 125	13.8	9.9	30	2	US-09-019-201A-9	Sequence 9, Appl	C 198	13.2	9.5	19	1	US-08-486-962-16	Sequence 16, Appl
C 126	13.8	9.9	30	2	US-08-458-101-455	Sequence 455, Appl	C 199	13.2	9.5	19	5	US-08-486-962-16	Sequence 16, Appl
C 127	13.8	9.9	30	3	US-09-369-618-14	Sequence 14, Appl	C 200	13.2	9.5	20	1	US-07-696-793A-17	Sequence 17, Appl
C 128	13.8	9.9	30	3	US-09-369-618-14	Sequence 14, Appl	C 201	13.2	9.5	20	1	US-07-977-694-17	Sequence 17, Appl
C 129	13.8	9.9	30	3	US-09-881-037-103	Sequence 103, Appl	C 202	13.2	9.5	20	3	US-09-357-070-43	Sequence 43, Appl
C 130	13.8	9.9	30	3	US-09-021-701-587	Sequence 587, Appl	C 203	13.2	9.5	20	3	US-09-593-711A-114	Sequence 114, Appl
C 131	13.6	9.8	20	3	US-09-467-642-88	Sequence 88, Appl	C 204	13.2	9.5	20	3	US-09-742-703-19	Sequence 19, Appl
C 132	13.6	9.8	20	4	US-09-422-978-10402	Sequence 10402, A	C 205	13.2	9.5	20	4	US-09-198-452A-6149	Sequence 6149, Appl
C 133	13.6	9.8	20	4	US-09-198-452A-6657	Sequence 6657, A	C 206	13.2	9.5	20	4	US-08-288-405A-20	Sequence 20, Appl
C 134	13.6	9.8	20	4	US-09-198-452A-6714	Sequence 6714, A	C 207	13.2	9.5	21	1	US-08-145-658B-12	Sequence 12, Appl
C 135	13.6	9.8	20	3	US-08-577-081A-58	Sequence 58, Appl	C 208	13.2	9.5	21	2	US-09-744-022-7	Sequence 7, Appl
C 136	13.6	9.8	21	4	US-09-778-510-14	Sequence 14, Appl	C 209	13.2	9.5	21	4	US-09-422-978-7403	Sequence 7403, Appl
C 137	13.6	9.8	21	4	US-08-923-454A-15	Sequence 15, Appl	C 210	13.2	9.5	21	4	US-09-182-145-121	Sequence 121, Appl
C 138	13.6	9.8	25	1	US-08-306-254-1	Sequence 1, Appl	C 211	13.2	9.5	23	4	US-07-977-284A-73	Sequence 73, Appl
C 139	13.6	9.8	25	1	US-08-470-202-5	Sequence 5, Appl	C 212	13.2	9.5	24	1	US-08-256-426B-73	Sequence 73, Appl
C 140	13.6	9.8	25	2	US-08-468-059-5	Sequence 5, Appl	C 213	13.2	9.5	24	3	US-07-992-600-8	Sequence 8, Appl
C 141	13.6	9.8	25	3	US-09-109-916-5	Sequence 5, Appl	C 214	13.2	9.5	24	3	US-09-157-021-8	Sequence 8, Appl
C 142	13.6	9.8	25	4	US-09-886-156-5	Sequence 5, Appl	C 215	13.2	9.5	24	3	US-09-156-842-8	Sequence 8, Appl
C 143	13.6	9.8	25	4	US-09-886-149-5	Sequence 5, Appl	C 216	13.2	9.5	24	3	US-09-177-650-76	Sequence 76, Appl
C 144	13.6	9.8	25	4	US-09-886-159-5	Sequence 5, Appl	C 217	13.2	9.5	24	3	US-08-974-549A-423	Sequence 423, Appl
C 145	13.6	9.8	26	3	US-09-493-352A-2	Sequence 2, Appl	C 218	13.2	9.5	25	3	US-08-912-951-190	Sequence 190, Appl
C 146	13.6	9.8	26	4	US-09-493-351B-3	Sequence 3, Appl	C 219	13.2	9.5	25	4	US-08-093-741-53	Sequence 53, Appl
C 147	13.6	9.8	27	2	US-08-500-857A-17	Sequence 17, Appl	C 220	13.2	9.5	26	1	US-08-720-012-53	Sequence 53, Appl
C 148	13.6	9.8	27	4	US-09-602-586-28	Sequence 28, Appl	C 221	13.2	9.5	26	2	US-08-859-998-349	Sequence 349, Appl
C 149	13.6	9.8	28	1	US-08-227-536-13	Sequence 13, Appl	C 222	13.2	9.5	26	4	US-09-225-928-349	Sequence 349, Appl
C 150	13.6	9.8	28	4	US-09-194-285-6	Sequence 6, Appl	C 223	13.2	9.5	26	4	US-09-202-904A-2	Sequence 2, Appl
C 151	13.6	9.8	28	5	PCT-US95-04682-13	Sequence 13, Appl	C 224	13.2	9.5	26	4	US-09-996-243-242	Sequence 242, Appl
C 152	13.6	9.8	29	3	US-09-295-028-78	Sequence 78, Appl	C 225	13.2	9.5	26	4	US-09-225-201B-349	Sequence 20, Appl
C 153	13.6	9.8	29	4	US-09-439-261-52	Sequence 52, Appl	C 226	13.2	9.5	26	4	US-09-109-329-20	Sequence 20, Appl
C 154	13.6	9.8	29	4	US-08-384-708A-170	Sequence 170, Appl	C 227	13.2	9.5	26	4	US-08-450-246-36	Sequence 36, Appl
C 155	13.6	9.8	30	1	US-08-640-517A-76	Sequence 76, Appl	C 228	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 156	13.6	9.8	30	2	US-08-860-882A-21	Sequence 21, Appl	C 229	13.2	9.5	27	1	US-08-451-233-36	Sequence 36, Appl
C 157	13.6	9.8	30	3	US-08-687-421-170	Sequence 170, Appl	C 230	13.2	9.5	27	1	US-08-451-233-36	Sequence 36, Appl
C 158	13.6	9.8	30	4	US-09-419-161-3	Sequence 3, Appl	C 231	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 159	13.6	9.8	30	4	US-09-011-769A-17	Sequence 17, Appl	C 232	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 160	13.6	9.8	30	4	US-09-428-583-84	Sequence 84, Appl	C 233	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 161	13.6	9.8	30	4	US-09-360-416-9	Sequence 9, Appl	C 234	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 162	13.6	9.8	30	4	US-08-482-174B-4	Sequence 4, Appl	C 235	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 163	13.6	9.8	30	4	US-08-632-662A-8	Sequence 8, Appl	C 236	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 164	13.6	9.8	30	4	US-08-631-554A-8	Sequence 8, Appl	C 237	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 165	13.6	9.8	30	4	US-09-103-153-8	Sequence 8, Appl	C 238	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 166	13.6	9.8	30	4	US-08-484-201A-4	Sequence 4, Appl	C 239	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 167	13.6	9.8	30	4	US-08-484-201A-4	Sequence 4, Appl	C 240	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 168	13.4	9.6	20	3	US-09-360-416-9	Sequence 9, Appl	C 241	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 169	13.4	9.6	20	4	US-08-482-174B-4	Sequence 4, Appl	C 242	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 170	13.4	9.6	23	1	US-08-632-662A-8	Sequence 8, Appl	C 243	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 171	13.4	9.6	23	2	US-08-631-554A-8	Sequence 8, Appl	C 244	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 172	13.4	9.6	23	2	US-09-103-153-8	Sequence 8, Appl	C 245	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl
C 173	13.4	9.6	23	2	US-08-484-201A-4	Sequence 4, Appl	C 246	13.2	9.5	27	1	US-08-450-098-36	Sequence 36, Appl

247	13.2	9.5	29	1	US-08-412-110-32	Sequence 32, Appl	C 320	12.8	9.2	4	US-09-371-772B-3692	Sequence 3692, Ap
248	13.2	9.5	29	1	US-08-409-442A-32	Sequence 32, Appl	C 321	12.8	9.2	5	PCT-US94-06284-12	Sequence 12, Appl
249	13.2	9.5	29	1	US-08-488-457-28	Sequence 28, Appl	C 322	12.8	9.2	18	US-08-486-962-15	Sequence 15, Appl
250	13.2	9.5	29	2	US-08-338-793D-28	Sequence 28, Appl	C 323	12.8	9.2	18	US-08-671-975A-7	Sequence 7, Appl
251	13.2	9.5	29	2	US-08-469-609A-32	Sequence 32, Appl	C 324	12.8	9.2	18	US-09-280-409-109	Sequence 109, App
252	13.2	9.5	29	3	US-09-143-190-32	Sequence 32, Appl	C 325	12.8	9.2	18	US-09-280-409-142	Sequence 142, App
253	13.2	9.5	29	4	US-09-238-356-45	Sequence 45, Appl	C 326	12.8	9.2	18	PCT-US94-06284-15	Sequence 15, Appl
254	13.2	9.5	29	4	US-09-238-356-45	Sequence 32, Appl	C 327	12.8	9.2	19	US-08-785-247-12	Sequence 12, Appl
255	13.2	9.5	29	4	US-09-502-34-32	Sequence 14, Appl	C 328	12.8	9.2	20	US-08-486-962-2	Sequence 2, Appl
C 256	13.2	9.5	29	4	US-07-672-530C-14	Sequence 23, Appl	C 329	12.8	9.2	20	US-09-021-701-441	Sequence 441, App
C 257	13.2	9.5	29	4	US-07-672-530C-23	Sequence 23, Appl	C 330	12.8	9.2	20	US-09-021-701-442	Sequence 442, App
C 258	13.2	9.5	30	2	US-08-995-927-8	Sequence 9, Appl	C 331	12.8	9.2	20	US-09-021-701-443	Sequence 443, App
C 259	13.2	9.5	30	3	US-08-895-707-12	Sequence 12, Appl	C 332	12.8	9.2	20	US-09-021-701-444	Sequence 444, App
C 260	13.2	9.5	30	3	US-09-432-335-9	Sequence 9, Appl	C 333	12.8	9.2	20	US-09-021-701-445	Sequence 445, App
C 261	13.2	9.5	30	3	US-09-432-335-9	Sequence 12, Appl	C 334	12.8	9.2	20	US-09-661-753-56	Sequence 56, Appl
C 262	13.2	9.5	30	4	US-09-582-096-8	Sequence 8, Appl	C 335	12.8	9.2	20	US-09-422-978-6924	Sequence 624, Ap
C 263	13.2	9.5	30	4	US-09-608-706-1	Sequence 1, Appl	C 336	12.8	9.2	20	US-09-198-452A-4511	Sequence 4511, Ap
C 264	13.2	9.5	30	4	US-09-614-022-9	Sequence 9, Appl	C 337	12.8	9.2	22	US-09-177-650-39	Sequence 39, Appl
C 265	13.2	9.5	30	4	US-08-363-240A-758	Sequence 758, App	C 338	12.8	9.2	22	US-09-102-830-1	Sequence 1, Appl
C 266	13.2	9.5	30	4	US-08-363-240A-759	Sequence 759, App	C 339	12.8	9.2	23	US-08-810-599-21	Sequence 21, Appl
C 267	13.2	9.5	30	4	US-08-292-694A-45	Sequence 45, Appl	C 340	12.8	9.2	24	US-09-102-830-23	Sequence 23, Appl
C 268	13.2	9.5	30	4	US-08-292-694A-45	Sequence 19, Appl	C 341	12.8	9.2	24	US-08-757-438-1	Sequence 1, Appl
C 269	13.2	9.5	30	4	US-08-418-817-4	Sequence 4, Appl	C 342	12.8	9.2	24	US-09-305-681-47	Sequence 47, Appl
C 270	13.2	9.5	30	4	US-08-468-024B-19	Sequence 19, Appl	C 343	12.8	9.2	24	US-09-305-681-48	Sequence 48, Appl
C 271	13.2	9.5	30	4	US-08-187-757D-17	Sequence 17, Appl	C 344	12.8	9.2	24	US-09-396-243-481	Sequence 481, App
C 272	13.2	9.5	30	4	US-08-509-024-4	Sequence 4, Appl	C 345	12.8	9.2	24	US-09-678-174-1	Sequence 1, Appl
C 273	13.2	9.5	30	4	US-09-333-279-4	Sequence 4, Appl	C 346	12.8	9.2	24	US-08-485-602-8	Sequence 8, Appl
C 274	13.2	9.5	30	4	US-09-631-780-4	Sequence 4, Appl	C 347	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 275	13.2	9.5	30	4	US-08-358-344B-15	Sequence 15, Appl	C 348	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 276	13.2	9.5	30	4	US-08-513-974B-236	Sequence 236, App	C 349	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 277	13.2	9.5	30	4	US-09-338-907-472	Sequence 472, App	C 350	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 278	13.2	9.5	30	4	US-09-218-207-472	Sequence 472, App	C 351	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 279	13.2	9.5	30	4	US-08-284-768A-38	Sequence 38, Appl	C 352	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 280	13.2	9.5	30	4	US-08-898-517-15	Sequence 15, Appl	C 353	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 281	13.2	9.5	30	4	US-08-898-517-15	Sequence 15, Appl	C 354	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 282	13.2	9.5	30	4	US-08-214-770-17	Sequence 17, Appl	C 355	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 283	13.2	9.5	30	4	US-08-182-961B-40	Sequence 40, Appl	C 356	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 284	13.2	9.5	30	4	US-08-500-914A-25	Sequence 25, Appl	C 357	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 285	13.2	9.5	30	4	US-09-007-678B-40	Sequence 40, Appl	C 358	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 286	13.2	9.5	30	4	US-09-421-365-3	Sequence 3, Appl	C 359	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 287	13.2	9.5	30	4	PCT-US95-02885-17	Sequence 17, Appl	C 360	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 288	13.2	9.5	30	4	US-08-859-998-1221	Sequence 1221, Ap	C 361	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 289	13.2	9.5	30	4	US-09-225-928-1221	Sequence 1221, Ap	C 362	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 290	13.2	9.5	30	4	US-09-225-201B-1221	Sequence 1221, Ap	C 363	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 291	13.2	9.5	30	4	PCT-US94-06360-7	Sequence 7, Appl	C 364	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 292	13.2	9.5	30	4	US-08-444-732-12	Sequence 12, Appl	C 365	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 293	13.2	9.5	30	4	US-08-445-042-12	Sequence 12, Appl	C 366	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 294	13.2	9.5	30	4	US-08-513-974B-79	Sequence 79, Appl	C 367	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 295	13.2	9.5	30	4	US-09-253-396A-29	Sequence 29, Appl	C 368	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 296	13.2	9.5	30	4	US-09-475-316A-95	Sequence 95, Appl	C 369	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 297	13.2	9.5	30	4	US-09-475-316A-96	Sequence 96, Appl	C 370	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 298	13.2	9.5	30	4	US-08-679-645-1105	Sequence 1105, Ap	C 371	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 299	13.2	9.5	30	4	US-09-120-365-8	Sequence 8, Appl	C 372	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 300	13.2	9.5	30	4	US-09-515-039-8	Sequence 8, Appl	C 373	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 301	13.2	9.5	30	4	US-08-339-152A-5	Sequence 5, Appl	C 374	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 302	13.2	9.5	30	4	US-08-824-692-18	Sequence 18, Appl	C 375	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 303	13.2	9.5	30	4	US-09-304-332-822	Sequence 822, App	C 376	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 304	13.2	9.5	30	4	US-09-387-286-40	Sequence 40, Appl	C 377	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 305	13.2	9.5	30	4	US-08-219-012-50	Sequence 50, Appl	C 378	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 306	13.2	9.5	30	4	US-08-479-485-2	Sequence 2, Appl	C 379	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 307	13.2	9.5	30	4	US-08-186-329-35	Sequence 35, Appl	C 380	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 308	13.2	9.5	30	4	US-08-802-427-14	Sequence 14, Appl	C 381	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 309	13.2	9.5	30	4	US-08-470-124-35	Sequence 35, Appl	C 382	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 310	13.2	9.5	30	4	US-08-117-952-635	Sequence 635, App	C 383	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 311	13.2	9.5	30	4	US-08-588-983-37	Sequence 37, Appl	C 384	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 312	13.2	9.5	30	4	US-08-588-976-37	Sequence 37, Appl	C 385	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 313	13.2	9.5	30	4	US-08-589-028-17	Sequence 17, Appl	C 386	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 314	13.2	9.5	30	4	US-08-784-582-17	Sequence 17, Appl	C 387	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 315	13.2	9.5	30	4	US-08-513-974B-124	Sequence 124, App	C 388	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 316	13.2	9.5	30	4	US-08-687-421-238	Sequence 238, App	C 389	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 317	13.2	9.5	30	4	US-08-785-271-17	Sequence 17, Appl	C 390	12.8	9.2	25	US-08-485-602-8	Sequence 8, Appl
C 318	12.8	9.2	28	2	US-09-593-359-10	Sequence 10, Appl	C 391	12.8	9.2	28	US-08-461-134-49	Sequence 49, Appl
C 319	12.8	9.2	28	2	US-08-486-962-12	Sequence 12, Appl	C 392	12.8	9.2	28	US-08-461-361-49	Sequence 49, Appl
					US-08-584-040-7909	Sequence 7909, Ap					US-08-149-097D-21	Sequence 21, Appl

C 393	12.8	9.2	28	2	US-08-485-910-49	Sequence 49, Appl	C 466	12.6	9.1	20	3	US-09-490-692-72	Sequence 72, Appl
C 394	12.8	9.2	28	2	US-08-988-128-17	Sequence 17, Appl	467	12.6	9.1	20	3	US-09-476-256-7	Sequence 7, Appl
C 395	12.8	9.2	28	3	US-07-794-396-3	Sequence 3, Appl	468	12.6	9.1	20	3	US-09-476-256-12	Sequence 12, Appl
C 396	12.8	9.2	28	3	US-08-949-386-21	Sequence 21, Appl	C 469	12.6	9.1	20	3	US-09-021-701-586	Sequence 586, App
C 397	12.8	9.2	28	3	US-08-450-562-21	Sequence 21, Appl	C 470	12.6	9.1	20	3	US-09-021-701-588	Sequence 588, App
C 398	12.8	9.2	28	3	US-09-091-899-1	Sequence 1, Appl	C 471	12.6	9.1	20	3	US-09-487-368A-41	Sequence 41, Appl
C 399	12.8	9.2	28	3	US-08-943-012B-16	Sequence 16, Appl	472	12.6	9.1	20	3	US-09-455-683-2	Sequence 2, Appl
C 400	12.8	9.2	28	4	US-08-984-709A-21	Sequence 21, Appl	C 473	12.6	9.1	20	3	US-09-066-641-33	Sequence 33, Appl
C 401	12.8	9.2	28	4	US-08-450-272-21	Sequence 21, Appl	C 474	12.6	9.1	20	4	US-09-371-674-6	Sequence 6, Appl
C 402	12.8	9.2	28	5	PCT-US92-11357-4	Sequence 4, Appl	C 475	12.6	9.1	20	4	US-09-255-154D-18	Sequence 18, Appl
C 403	12.8	9.2	28	5	PCT-US95-06266-33	Sequence 33, Appl	C 476	12.6	9.1	20	4	US-09-629-644A-41	Sequence 41, Appl
C 404	12.8	9.2	29	1	US-08-206-384-5	Sequence 5, Appl	C 477	12.6	9.1	20	4	US-09-198-452A-1642	Sequence 1642, Ap
C 405	12.8	9.2	29	1	US-08-196-103A-20	Sequence 20, Appl	C 478	12.6	9.1	20	4	US-09-198-452A-1814	Sequence 1814, Ap
C 406	12.8	9.2	29	1	US-08-357-396-20	Sequence 20, Appl	C 479	12.6	9.1	20	4	US-09-198-452A-4064	Sequence 4064, Ap
C 407	12.8	9.2	29	1	US-07-724-500B-5	Sequence 5, Appl	C 480	12.6	9.1	20	4	US-09-198-452A-4453	Sequence 4453, Ap
C 408	12.8	9.2	29	1	US-08-386-141-20	Sequence 20, Appl	C 481	12.6	9.1	21	1	US-08-306-254-2	Sequence 2, Appl
C 409	12.8	9.2	29	1	US-08-541-950B-12	Sequence 12, Appl	C 482	12.6	9.1	21	2	US-08-117-952-161	Sequence 161, App
C 410	12.8	9.2	29	3	US-08-461-418B-5	Sequence 5, Appl	C 483	12.6	9.1	21	3	US-09-159-274-21	Sequence 21, Appl
C 411	12.8	9.2	29	3	US-08-752-722-5	Sequence 5, Appl	C 484	12.6	9.1	21	3	US-08-943-731-568	Sequence 568, App
C 412	12.8	9.2	29	3	US-09-083-756A-12	Sequence 12, Appl	C 485	12.6	9.1	22	1	US-07-814-964-5	Sequence 5, Appl
C 413	12.8	9.2	29	4	US-09-255-899-5	Sequence 5, Appl	C 486	12.6	9.1	22	1	US-08-258-442-5	Sequence 5, Appl
C 414	12.8	9.2	29	4	US-09-304-232-308	Sequence 308, App	C 487	12.6	9.1	22	2	US-09-002-177-11	Sequence 11, Appl
C 415	12.8	9.2	29	4	US-09-304-232-424	Sequence 424, App	C 488	12.6	9.1	22	2	US-08-747-536-11	Sequence 11, Appl
C 416	12.8	9.2	29	4	US-09-304-232-610	Sequence 610, App	C 489	12.6	9.1	22	2	US-08-810-599-37	Sequence 37, Appl
C 417	12.8	9.2	29	4	US-09-304-232-706	Sequence 706, App	C 490	12.6	9.1	22	3	US-09-010-641-39	Sequence 39, Appl
C 418	12.8	9.2	29	4	US-09-304-232-707	Sequence 707, App	C 491	12.6	9.1	22	3	US-09-356-281-37	Sequence 37, Appl
C 419	12.8	9.2	29	5	US-09-325-601-5	Sequence 5, Appl	C 492	12.6	9.1	22	3	US-09-356-281-39	Sequence 39, Appl
C 420	12.8	9.2	29	5	PCT-US91-01822A-5	Sequence 5, Appl	C 493	12.6	9.1	22	4	US-09-374-584-11	Sequence 11, Appl
C 421	12.8	9.2	29	5	PCT-US91-02628-5	Sequence 5, Appl	C 494	12.6	9.1	22	4	US-09-302-681-23	Sequence 23, Appl
C 422	12.8	9.2	29	5	PCT-US93-08329-2	Sequence 2, Appl	C 495	12.6	9.1	22	4	US-09-305-856B-113	Sequence 113, App
C 423	12.8	9.2	30	1	US-07-915-922-6	Sequence 6, Appl	C 496	12.6	9.1	22	5	PCT-US92-11107-5	Sequence 5, Appl
C 424	12.8	9.2	30	1	US-08-186-229-46	Sequence 46, Appl	C 497	12.6	9.1	23	1	US-07-841-662-8	Sequence 8, Appl
C 425	12.8	9.2	30	1	US-08-425-726-5	Sequence 5, Appl	C 498	12.6	9.1	23	1	US-08-209-797-8	Sequence 8, Appl
C 426	12.8	9.2	30	2	US-08-470-124-46	Sequence 46, App	C 499	12.6	9.1	23	1	US-08-669-685-8	Sequence 20, App
C 427	12.8	9.2	30	2	US-08-117-952-559	Sequence 559, App	C 500	12.6	9.1	23	2	US-08-822-028-20	Sequence 20, App
C 428	12.8	9.2	30	2	US-08-362-284-21	Sequence 21, Appl	C 501	12.6	9.1	23	2	US-08-822-028-33	Sequence 33, Appl
C 429	12.8	9.2	30	3	US-08-946-138-11	Sequence 11, Appl	C 502	12.6	9.1	23	2	US-09-103-486-8	Sequence 8, Appl
C 430	12.8	9.2	30	3	US-08-946-138-22	Sequence 22, Appl	C 503	12.6	9.1	23	3	US-08-479-285-20	Sequence 20, Appl
C 431	12.8	9.2	30	3	US-08-666-354A-8	Sequence 8, Appl	C 504	12.6	9.1	23	3	US-08-479-285-33	Sequence 33, Appl
C 432	12.8	9.2	30	3	US-08-513-974B-128	Sequence 128, App	C 505	12.6	9.1	23	3	US-09-039-982A-8	Sequence 8, Appl
C 433	12.8	9.2	30	3	US-08-513-974B-130	Sequence 130, App	C 506	12.6	9.1	23	3	US-09-039-641-8	Sequence 8, Appl
C 434	12.8	9.2	30	3	US-08-513-974B-131	Sequence 131, App	C 507	12.6	9.1	23	3	US-09-039-762A-8	Sequence 8, Appl
C 435	12.8	9.2	30	3	US-08-513-974B-132	Sequence 132, App	C 508	12.6	9.1	23	3	US-09-042-492D-8	Sequence 8, Appl
C 436	12.8	9.2	30	3	US-08-513-974B-139	Sequence 139, App	C 509	12.6	9.1	23	4	US-08-943-612A-8	Sequence 8, Appl
C 437	12.8	9.2	30	3	US-08-513-974B-142	Sequence 142, App	C 510	12.6	9.1	23	5	PCT-US93-01557-8	Sequence 25, Appl
C 438	12.8	9.2	30	3	US-08-647-924-23	Sequence 23, Appl	C 511	12.6	9.1	24	1	US-08-546-130A-25	Sequence 14, Appl
C 439	12.8	9.2	30	3	US-09-130-546D-11	Sequence 11, Appl	C 512	12.6	9.1	24	2	US-08-273-146-14	Sequence 13, Appl
C 440	12.8	9.2	30	3	US-09-130-546D-22	Sequence 22, Appl	C 513	12.6	9.1	24	2	US-08-680-395-33	Sequence 33, Appl
C 441	12.8	9.2	30	4	US-09-414-276-15	Sequence 15, Appl	C 514	12.6	9.1	24	3	US-08-513-974B-15	Sequence 15, Appl
C 442	12.8	9.2	30	4	US-09-355-912A-6	Sequence 6, Appl	C 515	12.6	9.1	24	3	US-08-513-974B-230	Sequence 230, App
C 443	12.8	9.2	30	4	US-09-761-962A-46	Sequence 46, Appl	C 516	12.6	9.1	24	3	US-09-018-584A-87	Sequence 87, Appl
C 444	12.8	9.2	30	4	US-09-227-694B-11	Sequence 11, Appl	C 517	12.6	9.1	24	3	US-09-066-641-13	Sequence 13, Appl
C 445	12.8	9.2	30	4	US-09-227-694B-22	Sequence 22, Appl	C 518	12.6	9.1	24	4	US-09-461-436B-15	Sequence 15, Appl
C 446	12.8	9.2	30	4	US-09-446-081-13	Sequence 13, Appl	C 519	12.6	9.1	24	4	US-08-117-952-566	Sequence 566, App
C 447	12.8	9.2	30	4	US-09-446-081-24	Sequence 24, Appl	C 520	12.6	9.1	25	2	US-08-053-451B-154	Sequence 36, Appl
C 448	12.8	9.2	30	4	US-09-119-507B-52	Sequence 52, Appl	C 521	12.6	9.1	25	3	US-09-010-641-36	Sequence 36, Appl
C 449	12.8	9.2	30	4	US-09-119-507B-109	Sequence 109, App	C 522	12.6	9.1	25	3	US-09-356-281-36	Sequence 2, Appl
C 450	12.8	9.2	30	4	US-08-897-556A-52	Sequence 52, Appl	C 523	12.6	9.1	26	2	US-09-028-361A-2	Sequence 13, Appl
C 451	12.6	9.1	19	2	US-08-267-803B-68	Sequence 68, Appl	C 524	12.6	9.1	26	3	US-09-267-311-5	Sequence 5, Appl
C 452	12.6	9.1	19	4	US-09-422-978-8278	Sequence 8278, Ap	C 525	12.6	9.1	26	4	US-08-626-169-13	Sequence 13, Appl
C 453	12.6	9.1	20	1	US-08-033-081B-14	Sequence 14, Appl	C 526	12.6	9.1	27	2	US-08-520-678A-10	Sequence 10, Appl
C 454	12.6	9.1	20	1	US-08-310-429A-4	Sequence 4, Appl	C 527	12.6	9.1	27	2	US-08-682-423A-4	Sequence 4, Appl
C 455	12.6	9.1	20	1	US-08-310-429A-9	Sequence 9, Appl	C 528	12.6	9.1	27	3	US-09-129-888-5	Sequence 5, Appl
C 456	12.6	9.1	20	1	US-08-531-556-105	Sequence 105, App	C 529	12.6	9.1	27	3	US-09-164-907-13	Sequence 13, Appl
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1 US-07-977-284A-75
1 US-07-665-960A-6
1 US-08-106-802-6
1 US-08-488-212A-46
1 US-08-066-325-14
1 US-08-474-450A-44
1 US-08-320-306-46
1 US-08-488-209B-46

Sequence 16, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 149, App
Sequence 152, App
Sequence 630, App
Sequence 26, Appl
Sequence 9, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 58, Appl
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Sequence 191, App
Sequence 149, App
Sequence 152, App
Sequence 11, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 15, Appl
Sequence 9, Appl
Sequence 1709, Ap
Sequence 6, Appl
Sequence 13, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 142, App
Sequence 46, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 111, App
Sequence 46, Appl
Sequence 49, Appl
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Sequence 5, Appl
Sequence 20, Appl
Sequence 71, Appl
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Sequence 2459, Ap
Sequence 4039, Ap
Sequence 12, Appl
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Sequence 75, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 46, Appl
Sequence 14, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 46, Appl

831	12.2	8.8	21	2	US-08-408-011-46	Sequence 46, Appl	C 904	12.2	8.8	25	4	US-09-498-074-35	Sequence 35, Appl
832	12.2	8.8	21	2	US-08-256-426B-75	Sequence 75, Appl	C 905	12.2	8.8	25	4	US-09-919-622A-4	Sequence 4, Appl
833	12.2	8.8	21	2	US-08-703-136-6	Sequence 6, Appl	C 906	12.2	8.8	25	4	US-08-153-051B-33	Sequence 33, Appl
834	12.2	8.8	21	3	US-08-846-111D-13	Sequence 13, Appl	C 907	12.2	8.8	26	1	US-08-060-952C-23	Sequence 23, Appl
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836	12.2	8.8	21	3	US-08-983-468-75	Sequence 75, Appl	C 909	12.2	8.8	26	1	US-08-151-477A-33	Sequence 33, Appl
837	12.2	8.8	21	3	US-09-397-992A-8	Sequence 8, Appl	C 910	12.2	8.8	26	2	US-08-117-952-30	Sequence 30, Appl
838	12.2	8.8	21	4	US-09-608-288A-36	Sequence 36, Appl	C 911	12.2	8.8	26	2	US-08-456-460C-16	Sequence 16, Appl
839	12.2	8.8	21	4	US-09-425-043-36	Sequence 36, Appl	C 912	12.2	8.8	26	2	US-08-859-998-539	Sequence 539, Appl
840	12.2	8.8	21	4	US-09-397-168-54	Sequence 54, Appl	C 913	12.2	8.8	26	2	US-09-009-895-5	Sequence 5, Appl
841	12.2	8.8	21	4	US-09-443-077-13	Sequence 13, Appl	C 914	12.2	8.8	26	3	US-09-380-696A-11	Sequence 11, Appl
842	12.2	8.8	21	4	US-09-457-066-41	Sequence 41, Appl	C 915	12.2	8.8	26	3	US-09-325-928-539	Sequence 539, Appl
843	12.2	8.8	21	4	US-09-370-268-36	Sequence 36, Appl	C 916	12.2	8.8	26	4	US-08-464-011B-23	Sequence 23, Appl
844	12.2	8.8	21	4	US-09-557-800C-36	Sequence 36, Appl	C 917	12.2	8.8	26	4	US-09-548-372D-49	Sequence 49, Appl
845	12.2	8.8	21	4	US-09-706-968-41	Sequence 41, Appl	C 918	12.2	8.8	26	4	US-09-548-367D-49	Sequence 49, Appl
846	12.2	8.8	21	4	US-09-422-978-7898	Sequence 7898, Ap	C 919	12.2	8.8	26	4	US-08-469-260A-682	Sequence 682, App
847	12.2	8.8	21	4	US-09-971-843-8	Sequence 8, Appl	C 920	12.2	8.8	26	4	US-09-225-201B-539	Sequence 539, App
848	12.2	8.8	21	4	US-08-557-139-35	Sequence 35, Appl	C 921	12.2	8.8	26	4	US-09-551-853D-49	Sequence 49, Appl
849	12.2	8.8	22	1	US-08-332-562A-55	Sequence 55, Appl	C 922	12.2	8.8	26	4	US-09-378-535-11	Sequence 11, Appl
850	12.2	8.8	22	2	US-08-332-562A-56	Sequence 56, Appl	C 923	12.2	8.8	26	4	US-08-488-446-682	Sequence 682, App
851	12.2	8.8	22	4	US-09-302-895-8	Sequence 8, Appl	C 924	12.2	8.8	26	4	US-09-466-028-18	Sequence 18, Appl
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853	12.2	8.8	23	1	US-08-219-842-65	Sequence 65, Appl	C 926	12.2	8.8	26	4	PCT-US94-0535A-16	Sequence 16, Appl
854	12.2	8.8	23	1	US-08-451-096-32	Sequence 32, Appl	C 927	12.2	8.8	26	5	US-08-290-448A-46	Sequence 46, Appl
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858	12.2	8.8	23	3	US-08-413-740A-35	Sequence 35, Appl	C 931	12.2	8.8	27	1	US-08-400-115-11	Sequence 11, Appl
859	12.2	8.8	23	4	US-09-019-160-64	Sequence 64, Appl	C 932	12.2	8.8	27	2	US-08-985-998-499	Sequence 499, App
860	12.2	8.8	23	5	PCT-US95-04063-4	Sequence 4, Appl	C 933	12.2	8.8	27	3	US-08-985-162-1246	Sequence 1246, Ap
861	12.2	8.8	23	5	PCT-US95-04063-35	Sequence 35, Appl	C 934	12.2	8.8	27	3	US-08-513-974B-190	Sequence 190, App
862	12.2	8.8	24	1	US-08-105-483-415	Sequence 415, Appl	C 935	12.2	8.8	27	3	US-03-270-485-6	Sequence 6, Appl
863	12.2	8.8	24	1	US-08-219-633-24	Sequence 24, Appl	C 936	12.2	8.8	27	3	US-08-474-922A-5	Sequence 5, Appl
864	12.2	8.8	24	1	US-08-515-236-24	Sequence 24, Appl	C 937	12.2	8.8	27	3	US-09-253-396A-57	Sequence 57, Appl
865	12.2	8.8	24	1	US-08-709-209-415	Sequence 415, Appl	C 938	12.2	8.8	27	3	US-09-260-843-3	Sequence 3, Appl
866	12.2	8.8	24	1	US-08-303-275-123	Sequence 123, Appl	C 939	12.2	8.8	27	4	US-08-461-939B-46	Sequence 46, Appl
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869	12.2	8.8	24	1	US-08-784-289-5	Sequence 5, Appl	C 942	12.2	8.8	27	4	US-08-255-928-499	Sequence 499, App
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871	12.2	8.8	24	2	US-08-417-210A-76	Sequence 76, Appl	C 944	12.2	8.8	27	4	US-09-223-654-3	Sequence 3, Appl
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875	12.2	8.8	24	3	US-08-785-271-42	Sequence 42, Appl	C 948	12.2	8.8	27	4	Patent No. 5256770	Patent No. 5466668
876	12.2	8.8	24	3	US-09-327-229-30	Sequence 30, Appl	C 949	12.2	8.8	27	6	Sequence 341, App	Sequence 341, App
877	12.2	8.8	24	3	US-09-094-557-32	Sequence 32, Appl	C 950	12.2	8.8	27	6	Sequence 65, Appl	Sequence 65, Appl
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879	12.2	8.8	24	3	US-09-199-542B-36	Sequence 36, Appl	C 952	12.2	8.8	28	1	Sequence 341, App	Sequence 341, App
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896	12.2	8.8	25	4	US-09-225-928-687	Sequence 687, App	C 969	12.2	8.8	28	4	Sequence 42, Appl	Sequence 42, Appl
897	12.2	8.8	25	4	US-09-512-342-23	Sequence 23, Appl	C 970	12.2	8.8	28	4	Sequence 42, Appl	Sequence 42, Appl
898	12.2	8.8	25	4	US-09-538-709-408	Sequence 408, App	C 971	12.2	8.8	28	4	Sequence 42, Appl	Sequence 42, Appl
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900	12.2	8.8	25	4	US-09-586-376-27	Sequence 27, Appl	C 973	12.2	8.8	28	4	Sequence 42, Appl	Sequence 42, Appl
901	12.2	8.8	25	4	US-07-672-530C-12	Sequence 12, Appl	C 974	12.2	8.8	29	1	Sequence 42, Appl	Sequence 42, Appl
902	12.2	8.8	25	4	US-09-904-116-1	Sequence 1, Appl	C 975	12.2	8.8	29	1	Sequence 42, Appl	Sequence 42, Appl
903	12.2	8.8	25	4			C 976	12.2	8.8	29	1	Sequence 42, Appl	Sequence 42, Appl

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C 978	12.2	8.8	29	3	US-09-126-280-16	Sequence 16, Appl
C 979	12.2	8.8	29	4	US-09-225-928-394	Sequence 394, Appl
C 980	12.2	8.8	29	4	US-09-225-201B-394	Sequence 394, Appl
C 981	12.2	8.8	29	4	US-09-304-232-370	Sequence 270, Appl
C 982	12.2	8.8	29	4	US-09-304-232-305	Sequence 305, Appl
C 983	12.2	8.8	29	4	US-09-304-232-359	Sequence 359, Appl
C 984	12.2	8.8	29	4	US-09-304-232-433	Sequence 433, Appl
C 985	12.2	8.8	29	4	US-09-304-232-679	Sequence 679, Appl
C 986	12.2	8.8	29	4	US-09-304-232-696	Sequence 696, Appl
C 987	12.2	8.8	29	4	US-09-848-813-8	Sequence 8, Appl
C 988	12.2	8.8	29	5	PCT-US94-04190-10	Sequence 10, Appl
C 989	12.2	8.8	30	1	US-07-931-473B-12	Sequence 12, Appl
C 990	12.2	8.8	30	1	US-08-062-022-8	Sequence 8, Appl
C 991	12.2	8.8	30	1	US-07-714-131C-12	Sequence 12, Appl
C 992	12.2	8.8	30	1	US-08-219-012-31	Sequence 31, Appl
C 993	12.2	8.8	30	1	US-07-982-174-6	Sequence 6, Appl
C 994	12.2	8.8	30	1	US-08-495-743-8	Sequence 8, Appl
C 995	12.2	8.8	30	1	US-08-413-110-12	Sequence 12, Appl
C 996	12.2	8.8	30	1	US-08-403-442A-12	Sequence 12, Appl
C 997	12.2	8.8	30	1	US-08-493-739-8	Sequence 8, Appl
C 998	12.2	8.8	30	1	US-08-297-706-6	Sequence 6, Appl
C 999	12.2	8.8	30	1	US-08-495-741-8	Sequence 8, Appl
C 1000	12.2	8.8	30	1	US-08-475-000-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-363-240A-1125
; Sequence 1125, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1125:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-1125

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Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 3; Mismatches 0; Indels

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DB       1  GCUCACAGCUGGAACCCU 18

RESULT 2
US-08-558-823-11
; Sequence 11, Application US/08558823
; Patent No. 5876994
; GENERAL INFORMATION:
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Roelofs, Wendell L.
; APPLICANT: Miller, Stuart J.
; TITLE OF INVENTION: PHEROMONE DESATURASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,823
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rogalekij Esq., Peter
; REGISTRATION NUMBER: 38,601
; REFERENCE/DOCKET NUMBER: 19603/400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1634
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-558-823-11

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131,

;; TITLE OF INVENTION: Fertility and Pregnancy
;; FILE REFERENCE: P7345.2
;; CURRENT APPLICATION NUMBER: US/09/419.161
;; CURRENT FILING DATE: 1999-10-15
;; NUMBER OF SEQ ID NOS: 4
;; SEQ ID NO 1
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Chicken II GnrH
US-09-419-161-1

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Best Local Similarity 75.0%; Pred. No. 8.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 4
US-09-304-232-439/c
; Sequence 439, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated with
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304.232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084.641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 439
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BLAM1EX3 152
US-09-304-232-439

Query Match 11.8%; Score 16.4; DB 4; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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RESULT 5
US-08-927-219-102
; Sequence 102, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisa
; APPLICANT: Kaisaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; TITLE OF INVENTION: AND HNF-4ALPHA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,219
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/029,679
;; FILING DATE: 30-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/028,056
;; FILING DATE: 02-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/025,719
;; FILING DATE: 10-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: ARCD:272
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 102:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-927-219-102

Query Match 11.7%; Score 16.2; DB 3; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 ACCAGGCTCACAGCTGGGAACC 48
||||| ||||| ||||| ||||| |||||
Db 2 ACCAGACTCACAGCTGGAACC 22

RESULT 6
US-08-802-547-6/c
; Sequence 6, Application US/08802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/08/802,547
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 24129-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816-474-9050
; TELEFAX: 816-474-9057
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
US-08-802-547-6

Query Match 11.7%; Score 16.2; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCCTCAACTCTCCCTATCCT 126
Db 30 CTCCTCCCTCTCTCTCTCTCTCT 10

RESULT 7
US-08-712-357-6/c
; Sequence 6, Application US/08/712357
; Patent No. 5808037
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT
; TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,357
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
US-08-712-357-6

Query Match 11.7%; Score 16.2; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCCTCAACTCTCCCTATCCT 126
Db 30 CTCCTCCCTCTCTCTCTCTCTCT 10

RESULT 8
US-08-459-489-7/c
; Sequence 7, Application US/08459489
; Patent No. 5686574
; GENERAL INFORMATION:
; APPLICANT: David D. Moore et al.
; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,489
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/843,350
; FILING DATE: February 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/126001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-459-489-7

Query Match 11.2%; Score 15.6; DB 1; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCCCTGCTCTCTCTCTCAG 64
Db 30 TCAGGCTGCTGCTCTCTCTCTCTCTCAG 1

RESULT 9
US-08-458-686-7/c
; Sequence 7, Application US/08458686
; Patent No. 5710017
; GENERAL INFORMATION:
```

APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,686
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-686-7

Query Match 11.2%; Score 15.6; DB 1; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCTGCTCTCTCCACCCAG 64
Db 30 TCAGGCGTCTGCTCTCTCTCTCCACCCAG 1

RESULT 10
US-07-843-350C-7/c
Sequence 7, Application US/07843350C
Patent No. 5756448
GENERAL INFORMATION:
APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/843,350C
FILING DATE: February 26, 1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-843-350C-7

Query Match 11.2%; Score 15.6; DB 1; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCTGCTCTCTCCACCCAG 64
Db 30 TCAGGCGTCTGCTCTCTCTCTCCACCCAG 1

RESULT 11
PCT-US93-01559-7/c
Sequence 7, Application PC/TUS9301559
GENERAL INFORMATION:
APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED MOLECULES AND
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01559
FILING DATE: 19930222
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-01559-7

Query Match 11.2%; Score 15.6; DB 5; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;

Matches	21;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;
QY	35	TCACAGCTGGAACCCCTGGTGTCTCCTCCAG	64						
DB	30	TCAGGGCTGCTCTCTCTCTGTCACCTCCAG	1						
RESULT 12									
US-09-161-466-19									
; Sequence 19, Application US/09161466									
; Patent No. 6204025									
; GENERAL INFORMATION:									
; APPLICANT: LIU, QIANG									
; TITLE OF INVENTION: EXON-LINKING FOR DNA BASED DIAGNOSTICS									
; FILE REFERENCE: 2124-292									
; CURRENT APPLICATION NUMBER: US/09/161,466									
; CURRENT FILING DATE: 1998-09-28									
; EARLIER APPLICATION NUMBER: US 60/060319									
; EARLIER FILING DATE: 1997-09-29									
; NUMBER OF SEQ ID NOS: 24									
; SOFTWARE: Patent in Ver. 2.0 - beta									
; SEQ ID NO 19									
; LENGTH: 23									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-161-466-19									
Query Match									
Best Local Similarity 10.9%; Score 15.2; DB 3; Length 23;									
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	83	AGGACTACCGATGGAGATGAGAT	102						
DB	4	AGGAGGAGGAGATGGACAT	23						
RESULT 13									
US-08-946-138-24									
; Sequence 24, Application US/08946138									
; Patent No. 6013445									
; GENERAL INFORMATION:									
; APPLICANT: Glenn Albrecht, Sydney Brenner, David H. Lloyd									
; TITLE OF INVENTION: Massively Parallel Signature Sequencing by									
; TITLE OF INVENTION: Ligation of Encoded Adaptors									
; NUMBER OF SEQUENCES: 28									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.									
; STREET: 3832 Bay Center Place									
; CITY: Hayward									
; STATE: California									
; COUNTRY: USA									
; ZIP: 94545									
COMPUTER READABLE FORM:									
MEDIUM TYPE: 3.5 inch diskette									
COMPUTER: IBM compatible									
OPERATING SYSTEM: Windows 3.1/DOS 5.0									
SOFTWARE: Microsoft Word for Windows, vers. 2.0									
CURRENT APPLICATION DATA:									
APPLICATION NUMBER: US/08/946,138									
FILING DATE:									
CLASSIFICATION: 435									
PRIOR APPLICATION DATA:									
APPLICATION NUMBER: 08/689,587									
FILING DATE: 12-AUG-96									
PRIOR APPLICATION DATA:									
APPLICATION NUMBER: 08/659,453									
FILING DATE: 06-JUN-96									
ATTORNEY/AGENT INFORMATION:									
NAME: Stephen C. Macevicz									
REGISTRATION NUMBER: 30,285									
REFERENCE/DOCKET NUMBER: 808-lus									
TELECOMMUNICATION INFORMATION:									
TELEPHONE: (510) 670-9365									

```

; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Adaptor
; NAME/KEY: misc_feature
; LOCATION: (1)...(30)
; OTHER INFORMATION: n = A,T,C or G
US-09-227-694B-24

Query Match          10.9%; Score 15.2; DB 4; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGC 56
      |||||
Db       6 ACAGCTGCATCCCTGGTGAC 25

RESULT 16
US-09-446-081-26
; Sequence 26, Application US/09446081
; Patent No. 6518023
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; TITLE OF INVENTION: High resolution physical maps of genomic DNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/446,081
; FILING DATE: 27-Mar-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/884,189
; FILING DATE: 27-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent M. Powers
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 5525-0036.41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-446-081-26

Query Match          10.9%; Score 15.2; DB 4; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGC 56
      |||||
Db       6 ACAGCTGCATCCCTGGTGAC 25

RESULT 17
US-08-363-240A-240
```

```

; Sequence 240, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaler, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 240:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-240

Query Match          10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.7e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 TGGGGCTTGTAGCAG 18
      :|||:|:|:|:|:|:|
Db       1 UGGGGCUUGUACGAG 15

RESULT 18
US-08-363-240A-241
; Sequence 241, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaler, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-241

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCGTGTAGCAGAG 21
Db 1 GCGUUGAGCAGAG 15

RESULT 19
US-08-363-240A-242
Sequence 242, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A

FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-242

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 29 CCAGGCTCACAGCTG 43
Db 1 CCAGGCUCACAGCUG 15

RESULT 20
US-08-363-240A-243
Sequence 243, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:


```

; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-246

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 70 TCGAAGTTGGGTTAG 84
Db 1 UCGAGUUGGUAG 15

RESULT 24
US-08-363-240A-247
; Sequence 247, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-247

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GUUGGUUAGGAGUA 15

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; Sequence 248, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
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; ZIP: 90071
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; MEDIUM TYPE: storage
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-248
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; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: storage
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; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-246

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Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 70 TCGAAGTTGGGTTAG 84
Db 1 UCGAGUUGGUAG 15

RESULT 24
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; Sequence 247, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 32,327
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; TELEPHONE: (213) 489-1600
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; INFORMATION FOR SEQ ID NO: 247:
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; TOPOLOGY: linear
; US-08-363-240A-247
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; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-248

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Query Match      10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. NO. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 22, 2003, 11:46:22
Job time : 81 secs

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156	13.6	9.8	25	14	US-10-098-263B-15080	Sequence 15080, A	c 229	13.4	9.6	27	13	US-10-044-592-21	Sequence 21, Appl
157	13.6	9.8	25	14	US-10-098-263B-31205	Sequence 31205, A	c 230	13.4	9.6	27	13	US-10-067-477-8	Sequence 8, Appl
158	13.6	9.8	25	14	US-10-098-263B-32293	Sequence 32293, A	c 231	13.4	9.6	27	13	US-10-090-569-8	Sequence 8, Appl
159	13.6	9.8	25	14	US-10-098-263B-43529	Sequence 43529, A	c 232	13.4	9.6	27	14	US-10-001-546-63	Sequence 63, Appl
160	13.6	9.8	25	14	US-10-098-263B-55621	Sequence 55621, A	c 233	13.4	9.6	27	14	US-10-184-722-6	Sequence 6, Appl
161	13.6	9.8	25	14	US-10-098-263B-63516	Sequence 63516, A	c 234	13.4	9.6	27	14	US-10-245-801-2	Sequence 2, Appl
162	13.6	9.8	25	14	US-10-098-263B-81065	Sequence 81065, A	c 235	13.4	9.6	27	14	US-10-184-426-6	Sequence 6, Appl

236	13.4	9.6	29	10	US-09-736-960-122	Sequence 122, App	C 309	13.2	9.5	26	11	US-09-990-711-242	Sequence 242, App
237	13.4	9.6	29	11	US-09-374-046A-162	Sequence 162, App	C 310	13.2	9.5	26	11	US-09-989-726-242	Sequence 242, App
238	13.4	9.6	30	10	US-09-739-088-18	Sequence 10, Appl	C 311	13.2	9.5	26	11	US-09-998-156-242	Sequence 242, App
239	13.4	9.6	30	14	US-10-136-444-28	Sequence 28, Appl	C 312	13.2	9.5	26	11	US-09-990-437-242	Sequence 242, App
240	13.4	9.6	30	14	US-10-251-385-115	Sequence 115, App	C 313	13.2	9.5	26	11	US-09-991-157-242	Sequence 242, App
241	13.4	9.6	30	14	US-10-309-851-29	Sequence 29, Appl	C 314	13.2	9.5	26	11	US-09-997-514-242	Sequence 242, App
242	13.2	9.5	29	11	US-09-972-115A-27	Sequence 27, Appl	C 315	13.2	9.5	26	11	US-09-997-573-242	Sequence 242, App
243	13.2	9.5	20	10	US-09-745-605-16	Sequence 16, Appl	C 316	13.2	9.5	26	11	US-09-991-172-242	Sequence 242, App
244	13.2	9.5	20	10	US-09-969-373-1709	Sequence 1709, App	C 317	13.2	9.5	26	11	US-09-990-726-242	Sequence 242, App
245	13.2	9.5	21	14	US-10-066-191-68	Sequence 68, Appl	C 318	13.2	9.5	26	11	US-09-997-559-242	Sequence 242, App
246	13.2	9.5	22	14	US-10-194-370-16	Sequence 16, Appl	C 319	13.2	9.5	26	11	US-09-997-601-242	Sequence 242, App
247	13.2	9.5	22	14	US-10-216-540-4	Sequence 4, Appl	C 320	13.2	9.5	26	11	US-09-990-443-242	Sequence 242, App
248	13.2	9.5	23	8	US-08-913-430-17	Sequence 17, Appl	C 321	13.2	9.5	26	11	US-09-991-854-242	Sequence 242, App
249	13.2	9.5	23	14	US-10-112-267-121	Sequence 121, App	C 322	13.2	9.5	26	11	US-09-997-628-242	Sequence 242, App
250	13.2	9.5	24	11	US-08-854-140-6	Sequence 6, Appl	C 323	13.2	9.5	26	11	US-09-997-683-242	Sequence 242, App
251	13.2	9.5	24	11	US-09-940-185-674	Sequence 674, App	C 324	13.2	9.5	26	11	US-09-989-729A-242	Sequence 242, App
252	13.2	9.5	24	11	US-09-940-185-3270	Sequence 3270, App	C 325	13.2	9.5	26	11	US-09-997-349-242	Sequence 242, App
253	13.2	9.5	25	9	US-09-866-108-3324	Sequence 3324, App	C 326	13.2	9.5	26	11	US-09-990-440-242	Sequence 242, App
254	13.2	9.5	25	9	US-09-866-108-3457	Sequence 3457, App	C 327	13.2	9.5	26	11	US-09-993-469-242	Sequence 242, App
255	13.2	9.5	25	9	US-09-866-108-3458	Sequence 3458, App	C 328	13.2	9.5	26	11	US-09-997-542-242	Sequence 242, App
256	13.2	9.5	25	9	US-09-866-108-3459	Sequence 3459, App	C 329	13.2	9.5	26	11	US-09-993-748-242	Sequence 242, App
257	13.2	9.5	25	9	US-09-866-108-3460	Sequence 3460, App	C 330	13.2	9.5	26	11	US-09-990-439-242	Sequence 242, App
258	13.2	9.5	25	9	US-09-866-108-3461	Sequence 3461, App	C 331	13.2	9.5	26	11	US-09-990-427-242	Sequence 242, App
259	13.2	9.5	25	9	US-09-866-108-3462	Sequence 3462, App	C 332	13.2	9.5	26	11	US-09-989-328-242	Sequence 242, App
260	13.2	9.5	25	9	US-09-866-108-3463	Sequence 3463, App	C 333	13.2	9.5	26	11	US-09-993-583-242	Sequence 242, App
261	13.2	9.5	25	9	US-09-866-108-3464	Sequence 3464, App	C 334	13.2	9.5	26	11	US-09-941-992-242	Sequence 242, App
262	13.2	9.5	25	11	US-09-992-665-248	Sequence 248, App	C 335	13.2	9.5	26	11	US-09-992-521-242	Sequence 242, App
263	13.2	9.5	25	11	US-09-940-185-4640	Sequence 4640, App	C 336	13.2	9.5	26	11	US-09-997-333-242	Sequence 242, App
264	13.2	9.5	25	14	US-10-215-112-2584	Sequence 2584, App	C 337	13.2	9.5	26	11	US-09-997-384-242	Sequence 242, App
265	13.2	9.5	25	14	US-10-044-692-190	Sequence 190, App	C 338	13.2	9.5	26	11	US-09-998-041-242	Sequence 242, App
266	13.2	9.5	25	14	US-10-098-263B-4849	Sequence 4849, App	C 339	13.2	9.5	26	11	US-09-997-585-242	Sequence 242, App
267	13.2	9.5	25	14	US-10-098-263B-30183	Sequence 30183, A	C 340	13.2	9.5	26	11	US-09-997-614-242	Sequence 242, App
268	13.2	9.5	25	14	US-10-098-263B-30581	Sequence 30581, A	C 341	13.2	9.5	26	11	US-09-989-862-242	Sequence 242, App
269	13.2	9.5	25	14	US-10-098-263B-31408	Sequence 31408, A	C 342	13.2	9.5	26	11	US-09-997-529-242	Sequence 242, App
270	13.2	9.5	25	14	US-10-098-263B-31880	Sequence 31880, A	C 343	13.2	9.5	26	11	US-10-244-718-3	Sequence 3, Appl
271	13.2	9.5	25	14	US-10-098-263B-50958	Sequence 50958, A	C 344	13.2	9.5	27	10	US-10-005-956-1216	Sequence 1216, App
272	13.2	9.5	25	14	US-10-098-263B-62268	Sequence 62268, A	C 345	13.2	9.5	27	10	US-09-235-594-7	Sequence 7, Appl
273	13.2	9.5	25	14	US-10-098-263B-62896	Sequence 62896, A	C 346	13.2	9.5	27	10	US-09-987-456-101	Sequence 101, App
274	13.2	9.5	25	14	US-10-098-263B-79540	Sequence 79540, A	C 347	13.2	9.5	27	10	US-09-818-991-55	Sequence 55, Appl
275	13.2	9.5	25	14	US-10-098-263B-94552	Sequence 94552, A	C 348	13.2	9.5	27	10	US-09-867-947-45	Sequence 45, Appl
276	13.2	9.5	25	14	US-10-098-263B-113613	Sequence 113613, A	C 349	13.2	9.5	27	10	US-10-061-395-90	Sequence 90, Appl
277	13.2	9.5	25	14	US-10-098-263B-113944	Sequence 113944, A	C 350	13.2	9.5	27	10	US-10-136-574-4	Sequence 4, Appl
278	13.2	9.5	25	14	US-10-098-263B-124517	Sequence 124517, A	C 351	13.2	9.5	27	10	US-10-302-557-14	Sequence 14, Appl
279	13.2	9.5	25	14	US-10-098-263B-130098	Sequence 130098, A	C 352	13.2	9.5	27	10	US-10-302-557-23	Sequence 23, Appl
280	13.2	9.5	25	14	US-09-118-276-16	Sequence 16, Appl	C 353	13.2	9.5	27	10	US-10-052-942-133	Sequence 133, Appl
281	13.2	9.5	26	9	US-09-989-722-242	Sequence 242, App	C 354	13.2	9.5	27	10	US-09-852-209A-30	Sequence 30, Appl
282	13.2	9.5	26	9	US-09-989-723-242	Sequence 242, App	C 355	13.2	9.5	27	10	US-10-146-255-4	Sequence 4, Appl
283	13.2	9.5	26	9	US-09-989-727-242	Sequence 242, App	C 356	13.2	9.5	27	10	US-10-241-476-16	Sequence 16, Appl
284	13.2	9.5	26	9	US-09-989-729-242	Sequence 242, App	C 357	13.2	9.5	27	10	US-10-085-906-203	Sequence 203, App
285	13.2	9.5	26	9	US-09-989-727-242	Sequence 242, App	C 358	13.2	9.5	27	10	US-10-131-600-30	Sequence 30, Appl
286	13.2	9.5	26	10	US-09-989-731-242	Sequence 242, App	C 359	13.2	9.5	27	10	US-09-877-478-2361	Sequence 2361, App
287	13.2	9.5	26	10	US-09-989-732-242	Sequence 242, App	C 360	13.2	9.5	27	10	US-09-983-531A-44	Sequence 44, Appl
288	13.2	9.5	26	10	US-09-991-073-242	Sequence 242, App	C 361	13.2	9.5	27	10	US-09-792-251-26	Sequence 26, Appl
289	13.2	9.5	26	10	US-09-990-442-242	Sequence 242, App	C 362	13.2	9.5	27	10	US-09-382-860-221	Sequence 221, App
290	13.2	9.5	26	10	US-09-991-163-242	Sequence 242, App	C 363	13.2	9.5	27	10	US-10-184-085A-293	Sequence 293, App
291	13.2	9.5	26	10	US-09-993-604-242	Sequence 242, App	C 364	13.2	9.5	27	10	US-10-079-429-19	Sequence 19, Appl
292	13.2	9.5	26	10	US-09-990-456-242	Sequence 242, App	C 365	13.2	9.5	27	10	US-10-848-990-12	Sequence 12, Appl
293	13.2	9.5	26	10	US-09-989-721-242	Sequence 242, App	C 366	13.2	9.5	27	10	US-09-924-231-4	Sequence 4, Appl
294	13.2	9.5	26	10	US-09-992-588-242	Sequence 242, App	C 367	13.2	9.5	27	10	US-09-925-673-3	Sequence 3, Appl
295	13.2	9.5	26	10	US-09-989-293A-242	Sequence 242, App	C 368	13.2	9.5	27	10	US-09-920-552-86	Sequence 86, Appl
296	13.2	9.5	26	10	US-09-989-735-242	Sequence 242, App	C 369	13.2	9.5	27	10	US-09-733-692A-12	Sequence 12, Appl
297	13.2	9.5	26	10	US-09-990-444-242	Sequence 242, App	C 370	13.2	9.5	27	10	US-09-940-185-1514	Sequence 1514, App
298	13.2	9.5	26	10	US-09-991-181-242	Sequence 242, App	C 371	13.2	9.5	27	10	US-09-940-185-1795	Sequence 1795, App
299	13.2	9.5	26	10	US-09-989-730-242	Sequence 242, App	C 372	13.2	9.5	27	10	US-09-940-185-2373	Sequence 2373, App
300	13.2	9.5	26	10	US-09-989-736-242	Sequence 242, App	C 373	13.2	9.5	27	10	US-09-940-185-2331	Sequence 3351, App
301	13.2	9.5	26	10	US-09-993-687-242	Sequence 242, App	C 374	13.2	9.5	27	10	US-10-072-094-38	Sequence 19, Appl
302	13.2	9.5	26	11	US-09-989-734-242	Sequence 242, App	C 375	13.2	9.5	27	10		
303	13.2	9.5	26	11	US-09-997-653-242	Sequence 242, App	C 376	13.2	9.5	27	10		
304	13.2	9.5	26	11	US-09-993-667-242	Sequence 242, App	C 377	13.2	9.5	27	10		
305	13.2	9.5	26	11	US-09-997-428-242	Sequence 242, App	C 378	13.2	9.5	27	10		
306	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 379	13.2	9.5	27	10		
307	13.2	9.5	26	11	US-09-990-438-242	Sequence 242, App	C 380	13.2	9.5	27	10		
308	13.2	9.5	26	11	US-09-990-562-242	Sequence 242, App	C 381	13.2	9.5	27	10		

C 382	13	9.4	25	9	US-09-866-108-4193	Sequence 4193, Ap	455	12.8	9.2	20	11	US-09-784-674-445	Sequence 445, App
C 383	13	9.4	25	9	US-09-866-108-4194	Sequence 4194, Ap	456	12.8	9.2	20	11	US-09-906-158-78	Sequence 78, Appl
C 384	13	9.4	25	9	US-09-866-108-4195	Sequence 4195, Ap	457	12.8	9.2	21	14	US-10-093-626B-5	Sequence 5, Appl
C 385	13	9.4	25	9	US-09-866-108-4196	Sequence 4196, Ap	458	12.8	9.2	24	9	US-09-989-722-481	Sequence 481, App
C 386	13	9.4	25	9	US-09-866-108-4197	Sequence 4197, Ap	459	12.8	9.2	24	9	US-09-989-723-481	Sequence 481, App
C 387	13	9.4	25	14	US-10-215-112-5293	Sequence 5293, Ap	460	12.8	9.2	24	9	US-09-989-279-481	Sequence 481, App
C 388	13	9.4	25	14	US-10-215-112-10959	Sequence 10959, A	461	12.8	9.2	24	9	US-09-989-727-481	Sequence 481, App
C 389	13	9.4	25	14	US-10-215-112-11510	Sequence 11510, A	462	12.8	9.2	24	10	US-09-989-731-481	Sequence 481, App
C 390	13	9.4	25	14	US-10-098-263B-4769	Sequence 4769, Ap	463	12.8	9.2	24	10	US-09-919-585-16	Sequence 16, Appl
C 391	13	9.4	25	14	US-10-098-263B-6706	Sequence 6706, Ap	464	12.8	9.2	24	10	US-09-989-732-481	Sequence 481, App
C 392	13	9.4	25	14	US-10-098-263B-8201	Sequence 8201, Ap	465	12.8	9.2	24	10	US-09-991-073-481	Sequence 481, App
C 393	13	9.4	25	14	US-10-098-263B-9802	Sequence 9802, Ap	466	12.8	9.2	24	10	US-09-990-442-481	Sequence 481, App
C 394	13	9.4	25	14	US-10-098-263B-9802	Sequence 9802, Ap	467	12.8	9.2	24	10	US-09-991-163-481	Sequence 481, App
C 395	13	9.4	25	14	US-10-098-263B-10438	Sequence 10438, A	468	12.8	9.2	24	10	US-09-993-604-481	Sequence 481, App
C 396	13	9.4	25	14	US-10-098-263B-14325	Sequence 14325, A	469	12.8	9.2	24	10	US-09-990-450-481	Sequence 481, App
C 397	13	9.4	25	14	US-10-098-263B-14326	Sequence 14326, A	470	12.8	9.2	24	10	US-09-989-727-481	Sequence 481, App
C 398	13	9.4	25	14	US-10-098-263B-14868	Sequence 14868, A	471	12.8	9.2	24	10	US-09-989-730-481	Sequence 481, App
C 399	13	9.4	25	14	US-10-098-263B-31323	Sequence 31323, A	472	12.8	9.2	24	10	US-09-992-598-481	Sequence 481, App
C 400	13	9.4	25	14	US-10-098-263B-31324	Sequence 31324, A	473	12.8	9.2	24	10	US-09-989-293A-481	Sequence 481, App
C 401	13	9.4	25	14	US-10-098-263B-38388	Sequence 38388, A	474	12.8	9.2	24	10	US-09-989-735-481	Sequence 481, App
C 402	13	9.4	25	14	US-10-098-263B-38419	Sequence 38419, A	475	12.8	9.2	24	10	US-09-990-444-481	Sequence 481, App
C 403	13	9.4	25	14	US-10-098-263B-42218	Sequence 42218, A	476	12.8	9.2	24	10	US-09-991-181-481	Sequence 481, App
C 404	13	9.4	25	14	US-10-098-263B-42888	Sequence 42888, A	477	12.8	9.2	24	10	US-09-989-730-481	Sequence 481, App
C 405	13	9.4	25	14	US-10-098-263B-47665	Sequence 47665, A	478	12.8	9.2	24	10	US-09-990-436-481	Sequence 481, App
C 406	13	9.4	25	14	US-10-098-263B-47666	Sequence 47666, A	479	12.8	9.2	24	10	US-09-993-687-481	Sequence 481, App
C 407	13	9.4	25	14	US-10-098-263B-56417	Sequence 56417, A	480	12.8	9.2	24	11	US-09-989-734-481	Sequence 481, App
C 408	13	9.4	25	14	US-10-098-263B-66712	Sequence 66712, A	481	12.8	9.2	24	11	US-09-883-152-104	Sequence 104, App
C 409	13	9.4	25	14	US-10-098-263B-68746	Sequence 68746, A	482	12.8	9.2	24	11	US-09-997-653-481	Sequence 481, App
C 410	13	9.4	25	14	US-10-098-263B-69725	Sequence 69725, A	483	12.8	9.2	24	11	US-09-993-667-481	Sequence 481, App
C 411	13	9.4	25	14	US-10-098-263B-72977	Sequence 72977, A	484	12.8	9.2	24	11	US-09-997-428-481	Sequence 481, App
C 412	13	9.4	25	14	US-10-098-263B-72978	Sequence 72978, A	485	12.8	9.2	24	11	US-09-997-666-481	Sequence 481, App
C 413	13	9.4	25	14	US-10-098-263B-73456	Sequence 73456, A	486	12.8	9.2	24	11	US-09-990-438-481	Sequence 481, App
C 414	13	9.4	25	14	US-10-098-263B-74596	Sequence 74596, A	487	12.8	9.2	24	11	US-09-990-562-481	Sequence 481, App
C 415	13	9.4	25	14	US-10-098-263B-82540	Sequence 82540, A	488	12.8	9.2	24	11	US-09-990-711-481	Sequence 481, App
C 416	13	9.4	25	14	US-10-098-263B-85470	Sequence 85470, A	489	12.8	9.2	24	11	US-09-989-726-481	Sequence 481, App
C 417	13	9.4	25	14	US-10-098-263B-87840	Sequence 87840, A	490	12.8	9.2	24	11	US-09-998-156-481	Sequence 481, App
C 418	13	9.4	25	14	US-10-098-263B-93186	Sequence 93186, A	491	12.8	9.2	24	11	US-09-990-437-481	Sequence 481, App
C 419	13	9.4	25	14	US-10-098-263B-98907	Sequence 98907, A	492	12.8	9.2	24	11	US-09-991-157-481	Sequence 481, App
C 420	13	9.4	25	14	US-10-098-263B-100503	Sequence 100503, A	493	12.8	9.2	24	11	US-09-997-514-481	Sequence 481, App
C 421	13	9.4	25	14	US-10-098-263B-102245	Sequence 102245, A	494	12.8	9.2	24	11	US-09-997-572-481	Sequence 481, App
C 422	13	9.4	25	14	US-10-098-263B-103872	Sequence 103872, A	495	12.8	9.2	24	11	US-09-991-173-481	Sequence 481, App
C 423	13	9.4	25	14	US-10-098-263B-109385	Sequence 109385, A	496	12.8	9.2	24	11	US-09-990-726-481	Sequence 481, App
C 424	13	9.4	25	14	US-10-098-263B-109385	Sequence 109385, A	497	12.8	9.2	24	11	US-09-997-559-481	Sequence 481, App
C 425	13	9.4	25	14	US-10-098-263B-110612	Sequence 110612, A	498	12.8	9.2	24	11	US-09-997-559-481	Sequence 481, App
C 426	13	9.4	25	14	US-10-098-263B-119684	Sequence 119684, A	499	12.8	9.2	24	11	US-09-997-601-481	Sequence 481, App
C 427	13	9.4	25	14	US-10-098-263B-120322	Sequence 120322, A	500	12.8	9.2	24	11	US-09-990-443-481	Sequence 481, App
C 428	13	9.4	25	14	US-10-098-263B-121395	Sequence 121395, A	501	12.8	9.2	24	11	US-09-991-854-481	Sequence 481, App
C 429	13	9.4	25	9	US-09-796-861-1	Sequence 3, Appl	502	12.8	9.2	24	11	US-09-997-628-481	Sequence 481, App
C 430	13	9.4	25	11	US-09-770-107-57	Sequence 1, Appl	503	12.8	9.2	24	11	US-09-997-683-481	Sequence 481, App
C 431	13	9.4	25	11	US-09-872-712-3	Sequence 57, Appl	504	12.8	9.2	24	11	US-09-989-729A-481	Sequence 481, App
C 432	13	9.4	25	14	US-10-010-476-76	Sequence 3, Appl	505	12.8	9.2	24	11	US-09-997-349-481	Sequence 481, App
C 433	13	9.4	25	10	US-09-758-269-19	Sequence 76, Appl	506	12.8	9.2	24	11	US-09-997-440-481	Sequence 481, App
C 434	13	9.4	25	11	US-09-961-077-1105	Sequence 19, Appl	507	12.8	9.2	24	11	US-09-993-469-481	Sequence 481, App
C 435	13	9.4	25	10	US-09-887-576-426	Sequence 1105, Ap	508	12.8	9.2	24	11	US-09-997-542-481	Sequence 481, App
C 436	13	9.4	25	14	US-10-169-580-11	Sequence 426, Ap	509	12.8	9.2	24	11	US-09-993-748-481	Sequence 481, App
C 437	13	9.4	25	9	US-10-300-341-40	Sequence 11, Appl	510	12.8	9.2	24	11	US-09-990-439-481	Sequence 481, App
C 438	13	9.4	25	14	US-10-079-384-38	Sequence 57, Appl	511	12.8	9.2	24	11	US-09-990-427-481	Sequence 481, App
C 439	13	9.4	25	9	US-09-771-425-3	Sequence 38, Appl	512	12.8	9.2	24	11	US-09-993-328-481	Sequence 481, App
C 440	13	9.4	25	9	US-09-874-138-9	Sequence 9, Appl	513	12.8	9.2	24	11	US-09-993-583-481	Sequence 481, App
C 441	13	9.4	25	13	US-10-005-842-9	Sequence 9, Appl	514	12.8	9.2	24	11	US-09-941-992-481	Sequence 481, App
C 442	13	9.4	25	13	US-10-085-906-100	Sequence 100, App	515	12.8	9.2	24	11	US-09-992-521-481	Sequence 481, App
C 443	13	9.4	25	17	US-09-877-478-994	Sequence 994, App	516	12.8	9.2	24	11	US-09-997-333-481	Sequence 481, App
C 444	12.8	9.2	17	11	US-09-877-478-1614	Sequence 1614, Ap	517	12.8	9.2	24	11	US-09-997-384-481	Sequence 481, App
C 445	12.8	9.2	17	11	US-09-848-754A-2544	Sequence 2544, Ap	518	12.8	9.2	24	11	US-09-940-185-156	Sequence 156, App
C 446	12.8	9.2	17	11	US-10-224-005-20	Sequence 20, Appl	519	12.8	9.2	24	11	US-09-940-185-2470	Sequence 2470, Ap
C 447	12.8	9.2	19	12	US-10-224-005-181	Sequence 181, App	520	12.8	9.2	24	11	US-09-940-185-3371	Sequence 3371, Ap
C 448	12.8	9.2	19	12	US-09-950-840-32	Sequence 32, Appl	521	12.8	9.2	24	11	US-09-982-860-192	Sequence 192, App
C 449	12.8	9.2	20	11	US-09-948-003-56	Sequence 56, Appl	522	12.8	9.2	24	11	US-09-988-041-481	Sequence 481, App
C 450	12.8	9.2	20	11	US-09-784-674-441	Sequence 441, App	523	12.8	9.2	24	11	US-09-997-585-481	Sequence 481, App
C 451	12.8	9.2	20	11	US-09-784-674-442	Sequence 442, App	524	12.8	9.2	24	11	US-09-997-614-481	Sequence 481, App
C 452	12.8	9.2	20	11	US-09-784-674-443	Sequence 443, App	525	12.8	9.2	24	12	US-09-989-862-481	Sequence 481, App
C 453	12.8	9.2	20	11	US-09-784-674-444	Sequence 444, App	526	12.8	9.2	24	12	US-09-989-725-481	Sequence 481, App
C 454	12.8	9.2	20	11	US-09-784-674-444	Sequence 444, App	527	12.8	9.2	24	12	US-09-997-529-481	Sequence 481, App

528	12.8	9.2	25	9	US-09-866-108-5773	Sequence 5773, App	12.8	9.2	27	10	US-09-817-014-168	Sequence 168, App
529	12.8	9.2	25	9	US-09-866-108-5774	Sequence 5774, App	12.8	9.2	28	14	US-10-225-630-21	Sequence 21, Appl
C 530	12.8	9.2	25	9	US-09-866-108-10947	Sequence 10947, App	12.8	9.2	29	10	US-09-972-016-1	Sequence 1, Appl
C 531	12.8	9.2	25	9	US-09-866-108-10948	Sequence 10948, App	12.8	9.2	30	9	US-09-766-399-42	Sequence 42, Appl
C 532	12.8	9.2	25	9	US-09-866-108-10949	Sequence 10949, App	12.8	9.2	30	9	US-09-908-130-5	Sequence 5, Appl
C 533	12.8	9.2	25	9	US-09-866-108-11169	Sequence 11169, App	12.8	9.2	30	9	US-09-908-130-16	Sequence 16, Appl
C 534	12.8	9.2	25	9	US-09-866-108-11170	Sequence 11170, App	12.8	9.2	30	9	US-09-908-131-5	Sequence 5, Appl
C 535	12.8	9.2	25	9	US-09-866-108-13691	Sequence 13691, App	12.8	9.2	30	9	US-09-908-131-16	Sequence 16, Appl
C 536	12.8	9.2	25	9	US-09-866-108-13692	Sequence 13692, App	12.8	9.2	30	9	US-09-908-131-16	Sequence 16, Appl
C 537	12.8	9.2	25	9	US-09-866-108-14096	Sequence 14096, App	12.8	9.2	30	9	US-09-761-963-46	Sequence 46, Appl
C 538	12.8	9.2	25	11	US-09-754-853A-508	Sequence 508, App	12.8	9.2	30	10	US-09-778-516A-3	Sequence 3, Appl
C 539	12.8	9.2	25	11	US-09-883-152-103	Sequence 103, App	12.8	9.2	30	10	US-09-907-795-16	Sequence 5, Appl
C 540	12.8	9.2	25	11	US-09-974-546-32	Sequence 32, Appl	12.8	9.2	30	10	US-09-907-795-16	Sequence 16, Appl
C 541	12.8	9.2	25	11	US-09-951-502A-13	Sequence 13, Appl	12.8	9.2	30	10	US-09-758-017A-12	Sequence 12, Appl
C 542	12.8	9.2	25	11	US-09-992-665-248	Sequence 248, App	12.8	9.2	30	10	US-09-963-875-31	Sequence 31, Appl
C 543	12.8	9.2	25	11	US-09-940-185-4137	Sequence 4137, App	12.8	9.2	30	14	US-10-136-891-23	Sequence 29, Appl
C 544	12.8	9.2	25	11	US-09-940-185-4647	Sequence 4647, App	12.8	9.2	30	14	US-10-087-714-16	Sequence 16, Appl
C 545	12.8	9.2	25	11	US-09-864-636A-1438	Sequence 1438, App	12.8	9.2	30	14	US-10-124-884-5	Sequence 5, Appl
C 546	12.8	9.2	25	11	US-09-864-636A-1438	Sequence 1438, App	12.8	9.2	30	14	US-10-124-884-16	Sequence 16, Appl
C 547	12.8	9.2	25	14	US-10-215-112-1810	Sequence 1810, App	12.8	9.2	30	14	US-10-151-336-15	Sequence 15, Appl
C 548	12.8	9.2	25	14	US-10-215-112-4287	Sequence 4287, App	12.8	9.2	30	14	US-10-120-687-31	Sequence 31, Appl
C 549	12.8	9.2	25	14	US-10-215-112-4797	Sequence 4797, App	12.8	9.2	30	14	US-10-202-428-6	Sequence 6, Appl
C 550	12.8	9.2	25	14	US-10-215-112-7458	Sequence 7458, App	12.8	9.2	30	14	US-10-283-300-46	Sequence 46, Appl
C 551	12.8	9.2	25	14	US-10-215-112-7584	Sequence 7584, App	12.8	9.2	30	14	US-08-983-605-55	Sequence 55, Appl
C 552	12.8	9.2	25	14	US-10-098-263B-6307	Sequence 6307, App	12.8	9.2	30	14	US-08-983-605-55	Sequence 40, Appl
C 553	12.8	9.2	25	14	US-10-098-263B-6567	Sequence 6567, App	12.8	9.2	30	14	US-08-731-499-40	Sequence 48, App
C 554	12.8	9.2	25	14	US-10-098-263B-21720	Sequence 2045, App	12.8	9.2	30	14	US-09-854-883-41	Sequence 41, Appl
C 555	12.8	9.2	25	14	US-10-098-263B-22771	Sequence 22771, App	12.8	9.2	30	14	US-09-773-307B-20	Sequence 20, Appl
C 556	12.8	9.2	25	14	US-10-098-263B-23963	Sequence 23963, App	12.8	9.2	30	11	US-09-931-375A-28	Sequence 28, Appl
C 557	12.8	9.2	25	14	US-10-098-263B-29237	Sequence 29237, App	12.8	9.2	30	11	US-09-802-640-51	Sequence 51, Appl
C 558	12.8	9.2	25	14	US-10-098-263B-33293	Sequence 33293, App	12.8	9.2	30	11	US-09-865-866-155	Sequence 155, App
C 559	12.8	9.2	25	14	US-10-098-263B-33294	Sequence 33294, App	12.8	9.2	30	11	US-09-784-674-586	Sequence 586, App
C 560	12.8	9.2	25	14	US-10-098-263B-33487	Sequence 33487, App	12.8	9.2	30	11	US-09-784-674-588	Sequence 588, App
C 561	12.8	9.2	25	14	US-10-098-263B-34452	Sequence 34452, App	12.8	9.2	30	11	US-09-952-522B-48	Sequence 48, Appl
C 562	12.8	9.2	25	14	US-10-098-263B-36864	Sequence 36864, App	12.8	9.2	30	12	US-10-020-478-66	Sequence 66, Appl
C 563	12.8	9.2	25	14	US-10-098-263B-38016	Sequence 38016, App	12.8	9.2	30	14	US-10-158-160A-50	Sequence 50, Appl
C 564	12.8	9.2	25	14	US-10-098-263B-41010	Sequence 41010, App	12.8	9.2	30	14	US-10-181-846-72	Sequence 72, Appl
C 565	12.8	9.2	25	14	US-10-098-263B-41486	Sequence 41486, App	12.8	9.2	30	14	US-10-213-452A-18	Sequence 18, Appl
C 566	12.8	9.2	25	14	US-10-098-263B-43881	Sequence 43881, App	12.8	9.2	30	14	US-09-765-081-398	Sequence 398, App
C 567	12.8	9.2	25	14	US-10-098-263B-59533	Sequence 59533, App	12.8	9.2	30	14	US-10-184-085A-399	Sequence 399, App
C 568	12.8	9.2	25	14	US-10-098-263B-60161	Sequence 60161, App	12.8	9.2	30	14	US-10-081-969-22	Sequence 22, Appl
C 569	12.8	9.2	25	14	US-10-098-263B-60672	Sequence 60672, App	12.8	9.2	30	14	US-10-081-969-67	Sequence 67, Appl
C 570	12.8	9.2	25	14	US-10-098-263B-63082	Sequence 63082, App	12.8	9.2	30	14	US-10-081-969-84	Sequence 84, Appl
C 571	12.8	9.2	25	14	US-10-098-263B-63583	Sequence 63583, App	12.8	9.2	30	14	US-09-305-856B-113	Sequence 113, Appl
C 572	12.8	9.2	25	14	US-10-098-263B-64259	Sequence 64259, App	12.8	9.2	30	10	US-09-966-880A-21	Sequence 21, Appl
C 573	12.8	9.2	25	14	US-10-098-263B-65413	Sequence 65413, App	12.8	9.2	30	12	US-10-266-463A-8	Sequence 8, Appl
C 574	12.8	9.2	25	14	US-10-098-263B-65507	Sequence 65507, App	12.8	9.2	30	12	US-10-105-200A-8	Sequence 8, Appl
C 575	12.8	9.2	25	14	US-10-098-263B-65508	Sequence 65508, App	12.8	9.2	30	14	US-10-105-504A-8	Sequence 8, Appl
C 576	12.8	9.2	25	14	US-10-098-263B-65508	Sequence 65508, App	12.8	9.2	30	14	US-10-105-504A-8	Sequence 8, Appl
C 577	12.8	9.2	25	14	US-10-098-263B-65508	Sequence 65508, App	12.8	9.2	30	14	US-08-731-499-37	Sequence 37, Appl
C 578	12.8	9.2	25	14	US-10-098-263B-66871	Sequence 66871, App	12.8	9.2	30	9	US-09-784-423-87	Sequence 87, Appl
C 579	12.8	9.2	25	14	US-10-098-263B-68215	Sequence 68215, App	12.8	9.2	30	11	US-09-940-185-1693	Sequence 1693, App
C 580	12.8	9.2	25	14	US-10-098-263B-68215	Sequence 68215, App	12.8	9.2	30	12	US-10-278-087A-15	Sequence 15, Appl
C 581	12.8	9.2	25	14	US-10-098-263B-74887	Sequence 74887, App	12.8	9.2	30	12	US-09-883-152-112	Sequence 112, App
C 582	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-215-112-5692	Sequence 5692, App
C 583	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-215-112-6455	Sequence 6455, App
C 584	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-215-112-6581	Sequence 6581, App
C 585	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-215-112-13966	Sequence 13966, App
C 586	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-352	Sequence 352, App
C 587	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-6901	Sequence 6901, App
C 588	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-6902	Sequence 6902, App
C 589	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 590	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 591	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 592	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 593	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 594	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 595	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 596	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 597	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 598	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 599	12.8	9.2	25	14	US-09-991-262-38	Sequence 38, Appl	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App
C 600	12.8	9.2	27	10	US-09-817-014-163	Sequence 163, Appl	12.8	9.2	30	14	US-10-098-263B-16234	Sequence 16234, App

C 674	12.6	9.1	25	14	US-10-098-263B-42319	Sequence 42319, A	C 747	12.6	9.1	30	15	US-10-219-935-7	Sequence 7, Appli
C 675	12.6	9.1	25	14	US-10-098-263B-42320	Sequence 42320, A	C 748	12.4	8.9	17	11	US-09-818-875-3470	Sequence 3470, Ap
C 676	12.6	9.1	25	14	US-10-098-263B-42321	Sequence 42321, A	C 749	12.4	8.9	17	11	US-09-818-875-3471	Sequence 3471, Ap
C 677	12.6	9.1	25	14	US-10-098-263B-43047	Sequence 43047, A	C 750	12.4	8.9	17	11	US-09-877-478-386	Sequence 386, App
C 678	12.6	9.1	25	14	US-10-098-263B-43048	Sequence 43048, A	C 751	12.4	8.9	17	11	US-09-827-395A-479	Sequence 395, App
C 679	12.6	9.1	25	14	US-10-098-263B-51824	Sequence 51824, A	C 752	12.4	8.9	17	11	US-09-827-395A-479	Sequence 395, App
C 680	12.6	9.1	25	14	US-10-098-263B-53457	Sequence 53457, A	C 753	12.4	8.9	17	11	US-09-827-395A-479	Sequence 395, App
C 681	12.6	9.1	25	14	US-10-098-263B-53458	Sequence 53458, A	C 754	12.4	8.9	18	10	US-09-827-395A-479	Sequence 395, App
C 682	12.6	9.1	25	14	US-10-098-263B-56727	Sequence 56727, A	C 755	12.4	8.9	18	10	US-09-827-395A-479	Sequence 395, App
C 683	12.6	9.1	25	14	US-10-098-263B-59013	Sequence 59013, A	C 756	12.4	8.9	18	10	US-09-827-395A-479	Sequence 395, App
C 684	12.6	9.1	25	14	US-10-098-263B-60646	Sequence 60646, A	C 757	12.4	8.9	18	10	US-09-827-395A-479	Sequence 395, App
C 685	12.6	9.1	25	14	US-10-098-263B-60647	Sequence 60647, A	C 758	12.4	8.9	19	11	US-09-827-395A-479	Sequence 395, App
C 686	12.6	9.1	25	14	US-10-098-263B-67854	Sequence 67854, A	C 759	12.4	8.9	20	10	US-09-827-395A-479	Sequence 395, App
C 687	12.6	9.1	25	14	US-10-098-263B-68517	Sequence 68517, A	C 760	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 688	12.6	9.1	25	14	US-10-098-263B-77270	Sequence 77270, A	C 761	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 689	12.6	9.1	25	14	US-10-098-263B-80624	Sequence 80624, A	C 762	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 690	12.6	9.1	25	14	US-10-098-263B-90659	Sequence 90659, A	C 763	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 691	12.6	9.1	25	14	US-10-098-263B-94422	Sequence 94422, A	C 764	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 692	12.6	9.1	25	14	US-10-098-263B-105219	Sequence 105219, A	C 765	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 693	12.6	9.1	25	14	US-10-098-263B-105219	Sequence 105219, A	C 766	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 694	12.6	9.1	25	14	US-10-098-263B-105219	Sequence 105219, A	C 767	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 695	12.6	9.1	25	14	US-10-098-263B-115270	Sequence 115270, A	C 768	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 696	12.6	9.1	25	14	US-10-098-263B-118660	Sequence 118660, A	C 769	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 697	12.6	9.1	25	14	US-10-098-263B-118904	Sequence 118904, A	C 770	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 698	12.6	9.1	25	14	US-10-098-263B-119249	Sequence 119249, A	C 771	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 699	12.6	9.1	25	14	US-10-098-263B-122343	Sequence 122343, A	C 772	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 700	12.6	9.1	25	14	US-10-098-263B-124966	Sequence 124966, A	C 773	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 701	12.6	9.1	26	11	US-09-439-429-13	Sequence 439, Appl	C 774	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 702	12.6	9.1	27	11	US-09-781-804-45	Sequence 781, Appl	C 775	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 703	12.6	9.1	27	11	US-09-880-508-10	Sequence 880, Appl	C 776	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 704	12.6	9.1	27	11	US-09-821-734-13	Sequence 821, Appl	C 777	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 705	12.6	9.1	27	12	US-10-337-993-17	Sequence 337, Appl	C 778	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 706	12.6	9.1	27	13	US-10-067-385-4	Sequence 67, Appl	C 779	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 707	12.6	9.1	27	14	US-10-158-314-10	Sequence 158, Appl	C 780	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 708	12.6	9.1	28	11	US-09-864-636A-847	Sequence 864, Appl	C 781	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 709	12.6	9.1	28	11	US-09-864-636A-848	Sequence 864, Appl	C 782	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 710	12.6	9.1	28	11	US-09-864-636A-849	Sequence 864, Appl	C 783	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 711	12.6	9.1	28	11	US-09-864-636A-850	Sequence 864, Appl	C 784	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 712	12.6	9.1	28	11	US-09-864-636A-851	Sequence 864, Appl	C 785	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 713	12.6	9.1	28	11	US-09-864-636A-852	Sequence 864, Appl	C 786	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 714	12.6	9.1	28	11	US-09-864-636A-853	Sequence 864, Appl	C 787	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 715	12.6	9.1	29	9	US-09-907-574-27	Sequence 907, Appl	C 788	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 716	12.6	9.1	29	9	US-09-839-649-2	Sequence 839, Appl	C 789	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 717	12.6	9.1	29	9	US-09-068-528B-27	Sequence 68, Appl	C 790	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 718	12.6	9.1	29	10	US-09-470-276-46	Sequence 47, Appl	C 791	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 719	12.6	9.1	29	11	US-09-927-737-19	Sequence 927, Appl	C 792	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 720	12.6	9.1	29	13	US-10-027-632-178113	Sequence 1027, Appl	C 793	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 721	12.6	9.1	29	13	US-10-027-632-178182	Sequence 1027, Appl	C 794	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 722	12.6	9.1	29	13	US-10-027-632-178205	Sequence 1027, Appl	C 795	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 723	12.6	9.1	29	13	US-10-027-632-178228	Sequence 1027, Appl	C 796	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 724	12.6	9.1	29	13	US-10-027-632-178251	Sequence 1027, Appl	C 797	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 725	12.6	9.1	29	14	US-10-060-990-52	Sequence 60, Appl	C 798	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 726	12.6	9.1	29	14	US-10-122-013-9	Sequence 122, Appl	C 799	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 727	12.6	9.1	29	14	US-10-265-590-2	Sequence 265, Appl	C 800	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 728	12.6	9.1	30	8	US-08-979-847-119	Sequence 979, Appl	C 801	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 729	12.6	9.1	30	9	US-09-862-915-4	Sequence 862, Appl	C 802	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 730	12.6	9.1	30	9	US-09-908-130-9	Sequence 908, Appl	C 803	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 731	12.6	9.1	30	9	US-09-882-507-7	Sequence 882, Appl	C 804	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 732	12.6	9.1	30	9	US-09-908-131-9	Sequence 908, Appl	C 805	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 733	12.6	9.1	30	10	US-09-881-823-32	Sequence 881, Appl	C 806	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 734	12.6	9.1	30	9	US-09-859-854-29	Sequence 859, Appl	C 807	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 735	12.6	9.1	30	10	US-09-924-112A-5	Sequence 924, Appl	C 808	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 736	12.6	9.1	30	10	US-09-971-798-9	Sequence 971, Appl	C 809	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 737	12.6	9.1	30	10	US-09-907-795-9	Sequence 907, Appl	C 810	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 738	12.6	9.1	30	11	US-09-852-416-29	Sequence 852, Appl	C 811	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 739	12.6	9.1	30	11	US-09-791-524-73	Sequence 791, Appl	C 812	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 740	12.6	9.1	30	12	US-10-302-840A-16	Sequence 302, Appl	C 813	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 741	12.6	9.1	30	14	US-10-004-551-108	Sequence 104, Appl	C 814	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 742	12.6	9.1	30	14	US-10-134-884-9	Sequence 134, Appl	C 815	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 743	12.6	9.1	30	14	US-10-096-790-8	Sequence 96, Appl	C 816	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 744	12.6	9.1	30	14	US-10-096-789-11	Sequence 96, Appl	C 817	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 745	12.6	9.1	30	14	US-10-270-071-40	Sequence 270, Appl	C 818	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App
C 746	12.6	9.1	30	14	US-10-270-071-54	Sequence 270, Appl	C 819	12.4	8.9	20	11	US-09-827-395A-479	Sequence 395, App

C 820	12.4	8.9	24	14	US-10-017-081A-93	Sequence 93, Appl	893	12.4	8.9	25	14	US-10-098-263B-43762	Sequence 43762, A
C 821	12.4	8.9	24	14	US-10-167-749-93	Sequence 93, Appl	C 894	12.4	8.9	25	14	US-10-098-263B-45883	Sequence 45883, A
C 822	12.4	8.9	24	14	US-10-095-672A-63	Sequence 63, Appl	C 895	12.4	8.9	25	14	US-10-098-263B-46375	Sequence 46375, A
C 823	12.4	8.9	24	14	US-10-095-672A-79	Sequence 79, Appl	C 896	12.4	8.9	25	14	US-10-098-263B-46993	Sequence 46993, A
C 824	12.4	8.9	24	14	US-10-013-921A-93	Sequence 93, Appl	C 897	12.4	8.9	25	14	US-10-098-263B-48583	Sequence 48583, A
C 825	12.4	8.9	24	14	US-10-013-929A-93	Sequence 93, Appl	C 898	12.4	8.9	25	14	US-10-098-263B-49447	Sequence 49447, A
C 826	12.4	8.9	24	14	US-10-016-177A-93	Sequence 93, Appl	C 899	12.4	8.9	25	14	US-10-098-263B-57769	Sequence 57769, A
C 827	12.4	8.9	24	14	US-10-166-709A-93	Sequence 93, Appl	900	12.4	8.9	25	14	US-10-098-263B-57770	Sequence 57770, A
C 828	12.4	8.9	25	9	US-09-866-108-4375	Sequence 4375, Ap	901	12.4	8.9	25	14	US-10-098-263B-61298	Sequence 61298, A
C 829	12.4	8.9	25	9	US-09-866-108-4376	Sequence 4376, Ap	902	12.4	8.9	25	14	US-10-098-263B-66287	Sequence 66287, A
C 830	12.4	8.9	25	9	US-09-866-108-4377	Sequence 4377, Ap	903	12.4	8.9	25	14	US-10-098-263B-66287	Sequence 66287, A
C 831	12.4	8.9	25	9	US-09-866-108-4378	Sequence 4378, Ap	C 904	12.4	8.9	25	14	US-10-098-263B-66795	Sequence 66795, A
C 832	12.4	8.9	25	9	US-09-866-108-4378	Sequence 4378, Ap	C 905	12.4	8.9	25	14	US-10-098-263B-66796	Sequence 66796, A
C 833	12.4	8.9	25	9	US-09-866-108-11280	Sequence 11280, A	C 906	12.4	8.9	25	14	US-10-098-263B-68475	Sequence 68475, A
C 834	12.4	8.9	25	9	US-09-866-108-11287	Sequence 11287, A	C 907	12.4	8.9	25	14	US-10-098-263B-68475	Sequence 68475, A
C 835	12.4	8.9	25	9	US-09-866-108-12968	Sequence 12968, A	C 908	12.4	8.9	25	14	US-10-098-263B-68899	Sequence 68899, A
C 836	12.4	8.9	25	9	US-09-866-108-12968	Sequence 12968, A	C 909	12.4	8.9	25	14	US-10-098-263B-69093	Sequence 69093, A
C 837	12.4	8.9	25	9	US-09-866-108-12970	Sequence 12970, A	C 910	12.4	8.9	25	14	US-10-098-263B-70346	Sequence 70346, A
C 838	12.4	8.9	25	9	US-09-866-108-12971	Sequence 12971, A	C 911	12.4	8.9	25	14	US-10-098-263B-71801	Sequence 71801, A
C 839	12.4	8.9	25	9	US-09-866-108-15099	Sequence 15099, A	C 912	12.4	8.9	25	14	US-10-098-263B-80749	Sequence 80749, A
C 840	12.4	8.9	25	9	US-09-866-108-15103	Sequence 15103, A	C 913	12.4	8.9	25	14	US-10-098-263B-82778	Sequence 82778, A
C 841	12.4	8.9	25	10	US-09-452-599-52	Sequence 52, Appl	C 914	12.4	8.9	25	14	US-10-098-263B-83342	Sequence 83342, A
C 842	12.4	8.9	25	10	US-09-528-175-33	Sequence 33, Appl	C 915	12.4	8.9	25	14	US-10-098-263B-83342	Sequence 83342, A
C 843	12.4	8.9	25	11	US-09-528-175-34	Sequence 34, Appl	C 916	12.4	8.9	25	14	US-10-098-263B-83938	Sequence 83938, A
C 844	12.4	8.9	25	11	US-09-754-853A-493	Sequence 493, Appl	C 917	12.4	8.9	25	14	US-10-098-263B-84857	Sequence 84857, A
C 845	12.4	8.9	25	11	US-09-754-853A-827	Sequence 827, Appl	C 918	12.4	8.9	25	14	US-10-098-263B-84858	Sequence 84858, A
C 846	12.4	8.9	25	11	US-09-883-152-107	Sequence 107, Appl	C 919	12.4	8.9	25	14	US-10-098-263B-86931	Sequence 86931, A
C 847	12.4	8.9	25	11	US-09-258-133-27	Sequence 27, Appl	C 920	12.4	8.9	25	14	US-10-098-263B-95443	Sequence 95443, A
C 848	12.4	8.9	25	11	US-09-269-921-41	Sequence 41, Appl	C 921	12.4	8.9	25	14	US-10-098-263B-95533	Sequence 95533, A
C 849	12.4	8.9	25	11	US-09-509-098-63	Sequence 63, Appl	C 922	12.4	8.9	25	14	US-10-098-263B-95885	Sequence 95885, A
C 850	12.4	8.9	25	14	US-10-076-597-29	Sequence 29, Appl	C 923	12.4	8.9	25	14	US-10-098-263B-98255	Sequence 98255, A
C 851	12.4	8.9	25	14	US-10-060-756A-2951	Sequence 2951, Ap	C 924	12.4	8.9	25	14	US-10-098-263B-98907	Sequence 98907, A
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C 853	12.4	8.9	25	14	US-10-215-112-2673	Sequence 2673, Ap	C 926	12.4	8.9	25	14	US-10-098-263B-100258	Sequence 100258, A
C 854	12.4	8.9	25	14	US-10-215-112-6072	Sequence 6072, Ap	C 927	12.4	8.9	25	14	US-10-098-263B-102451	Sequence 102451, A
C 855	12.4	8.9	25	14	US-10-215-112-6307	Sequence 6307, Ap	C 928	12.4	8.9	25	14	US-10-098-263B-102452	Sequence 102452, A
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C 858	12.4	8.9	25	14	US-10-215-112-8530	Sequence 8530, Ap	C 931	12.4	8.9	25	14	US-10-098-263B-106305	Sequence 106305, A
C 859	12.4	8.9	25	14	US-10-215-112-10856	Sequence 10856, A	C 932	12.4	8.9	25	14	US-10-098-263B-106468	Sequence 106468, A
C 860	12.4	8.9	25	14	US-10-215-112-11490	Sequence 11490, A	C 933	12.4	8.9	25	14	US-10-098-263B-106830	Sequence 106830, A
C 861	12.4	8.9	25	14	US-10-215-112-11503	Sequence 11503, A	C 934	12.4	8.9	25	14	US-10-098-263B-108066	Sequence 108066, A
C 862	12.4	8.9	25	14	US-10-215-112-11629	Sequence 11629, A	C 935	12.4	8.9	25	14	US-10-098-263B-110131	Sequence 110131, A
C 863	12.4	8.9	25	14	US-10-215-112-11823	Sequence 11823, A	C 936	12.4	8.9	25	14	US-10-098-263B-111247	Sequence 111247, A
C 864	12.4	8.9	25	14	US-10-215-112-13406	Sequence 13406, A	C 937	12.4	8.9	25	14	US-10-098-263B-112389	Sequence 112389, A
C 865	12.4	8.9	25	14	US-10-215-112-14317	Sequence 14317, A	C 938	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 866	12.4	8.9	25	14	US-10-215-112-14443	Sequence 14443, A	C 939	12.4	8.9	25	14	US-10-098-263B-116282	Sequence 116282, A
C 867	12.4	8.9	25	14	US-10-098-263B-3832	Sequence 3832, Ap	C 940	12.4	8.9	25	14	US-10-098-263B-117704	Sequence 117704, A
C 868	12.4	8.9	25	14	US-10-098-263B-3979	Sequence 3979, Ap	C 941	12.4	8.9	25	14	US-10-098-263B-120348	Sequence 120348, A
C 869	12.4	8.9	25	14	US-10-098-263B-5771	Sequence 5771, Ap	C 942	12.4	8.9	25	14	US-10-098-263B-122951	Sequence 122951, A
C 870	12.4	8.9	25	14	US-10-098-263B-8611	Sequence 8611, Ap	C 943	12.4	8.9	25	14	US-10-098-263B-124845	Sequence 124845, A
C 871	12.4	8.9	25	14	US-10-098-263B-14443	Sequence 14443, A	C 944	12.4	8.9	25	14	US-10-098-263B-124845	Sequence 124845, A
C 872	12.4	8.9	25	14	US-10-098-263B-16462	Sequence 16462, A	C 945	12.4	8.9	25	14	US-10-060-998-2219	Sequence 2219, Ap
C 873	12.4	8.9	25	14	US-10-098-263B-16827	Sequence 16827, A	C 946	12.4	8.9	25	14	US-10-060-998-2223	Sequence 2223, Ap
C 874	12.4	8.9	25	14	US-10-098-263B-19886	Sequence 19886, A	C 947	12.4	8.9	25	15	US-10-043-774B-8	Sequence 8, Appl
C 875	12.4	8.9	25	14	US-10-098-263B-22965	Sequence 22965, A	C 948	12.4	8.9	25	15	US-10-218-253-41	Sequence 41, Appl
C 876	12.4	8.9	25	14	US-10-098-263B-25173	Sequence 25173, A	C 949	12.4	8.9	26	13	US-09-970-989-36	Sequence 36, Appl
C 877	12.4	8.9	25	14	US-10-098-263B-27276	Sequence 27276, A	C 950	12.4	8.9	27	11	US-10-136-517-8	Sequence 8, Appl
C 878	12.4	8.9	25	14	US-10-098-263B-28941	Sequence 28941, A	C 951	12.4	8.9	27	11	US-09-872-712-16	Sequence 16, Appl
C 879	12.4	8.9	25	14	US-10-098-263B-30681	Sequence 30681, A	C 952	12.4	8.9	27	12	US-09-946-374-289	Sequence 289, App
C 880	12.4	8.9	25	14	US-10-098-263B-31688	Sequence 31688, A	C 953	12.4	8.9	27	12	US-10-015-387A-289	Sequence 289, App
C 881	12.4	8.9	25	14	US-10-098-263B-32305	Sequence 32305, A	C 954	12.4	8.9	27	12	US-10-006-130A-289	Sequence 289, App
C 882	12.4	8.9	25	14	US-10-098-263B-34350	Sequence 34350, A	C 955	12.4	8.9	27	14	US-10-006-172A-289	Sequence 289, App
C 883	12.4	8.9	25	14	US-10-098-263B-34797	Sequence 34797, A	C 956	12.4	8.9	27	14	US-10-006-856A-289	Sequence 289, App
C 884	12.4	8.9	25	14	US-10-098-263B-34988	Sequence 34988, A	C 957	12.4	8.9	27	14	US-10-006-818A-289	Sequence 289, App
C 885	12.4	8.9	25	14	US-10-098-263B-37693	Sequence 37693, A	C 958	12.4	8.9	27	14	US-10-015-387A-289	Sequence 289, App
C 886	12.4	8.9	25	14	US-10-098-263B-37684	Sequence 37684, A	C 959	12.4	8.9	27	14	US-10-015-869A-289	Sequence 289, App
C 887	12.4	8.9	25	14	US-10-098-263B-38244	Sequence 38244, A	C 960	12.4	8.9	27	14	US-10-012-121A-289	Sequence 289, App
C 888	12.4	8.9	25	14	US-10-098-263B-40196	Sequence 40196, A	C 961	12.4	8.9	27	14	US-10-006-116A-289	Sequence 289, App
C 889	12.4	8.9	25	14	US-10-098-263B-40745	Sequence 40745, A	C 962	12.4	8.9	27	14	US-10-006-117A-289	Sequence 289, App
C 890	12.4	8.9	25	14	US-10-098-263B-40865	Sequence 40865, A	C 963	12.4	8.9	27	14	US-10-017-527A-289	Sequence 289, App
C 891	12.4	8.9	25	14	US-10-098-263B-41776	Sequence 41776, A	C 964	12.4	8.9	27	14	US-10-013-913A-289	Sequence 289, App
C 892	12.4	8.9	25	14	US-10-098-263B-41966	Sequence 41966, A	C 965	12.4	8.9	27	14	US-10-007-194A-289	Sequence 289, App
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C 986 12.4 8.9 29 10 US-09-987-456-121
C 987 12.4 8.9 29 11 US-09-971-631-16
C 988 12.4 8.9 29 11 US-09-971-631-31
C 989 12.4 8.9 29 13 US-10-027-632-176475
C 990 12.4 8.9 29 14 US-10-215-432-42
C 991 12.4 8.9 30 9 US-09-818-068-15
C 992 12.4 8.9 30 11 US-09-815-981-3
C 993 12.4 8.9 30 11 US-09-948-747-28
C 994 12.4 8.9 30 11 US-09-815-979-3
C 995 12.4 8.9 30 11 US-09-992-665-359
C 996 12.4 8.9 30 11 US-09-769-878-19
C 997 12.4 8.9 30 13 US-10-073-353-7
C 998 12.4 8.9 30 14 US-10-085-906-122
C 999 12.4 8.9 30 14 US-10-267-900-9
1000 12.4 8.9 30 14 US-10-046-060A-19

ALIGNMENTS

RESULT 1
US-09-802-640-52/c
; Sequence 52, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Klevn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CARDIOVASCULAR DISEASE AND THEIR USE
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-802-640-52

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTGTAGCAGAGGCAAGCA 28
|||||
Db 20 CTGTAGCAGAGGCAAGCA 1

RESULT 2

US-09-925-139-5/c
; Sequence 5, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Pam Nero
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-925-139-5

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 65 CGTGTGGAAGTTGGGTTAG 84
|||||
Db 20 CGTGTGGAAGTTGGGTTAG 1

RESULT 3
US-09-925-139-28/c
; Sequence 28, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Pam Nero
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-28

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGATGGGCTTGTAGCAGAA 20
|||||
Db 20 GGATGGGCTTGTAGCAGAA 1

RESULT 4
US-09-925-139-29/c
; Sequence 29, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Pam Nero
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE

FILE REFERENCE: ISPH-0596
CURRENT APPLICATION NUMBER: US/09/925,139
CURRENT FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-29

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGGAACCTGGTGTCTCCT 60
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CTGGAACCTGGTGTCTCCT 1

RESULT 5

US-09-925-139-30/c
Sequence 30, Application US/09925139
Publication No. US20030092647A1
GENERAL INFORMATION:

APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
APPLICANT: Pam Nero
APPLICANT: Edward Wanciewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
FILE REFERENCE: ISPH-0596
CURRENT APPLICATION NUMBER: US/09/925,139
CURRENT FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-30

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GGAAGTGGTTAGGAGTAC 90
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGAAGTGGTTAGGAGTAC 1

RESULT 6

US-09-925-139-47/c
Sequence 47, Application US/09925139
Publication No. US20030092647A1
GENERAL INFORMATION:

APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
APPLICANT: Pam Nero
APPLICANT: Edward Wanciewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
FILE REFERENCE: ISPH-0596
CURRENT APPLICATION NUMBER: US/09/925,139
CURRENT FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-47

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGAGGCAAGC 27
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCTTGTAGCAGAGGCAAGC 1

RESULT 7

US-09-925-139-48/c
Sequence 48, Application US/09925139
Publication No. US20030092647A1
GENERAL INFORMATION:

APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
APPLICANT: Pam Nero
APPLICANT: Edward Wanciewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
FILE REFERENCE: ISPH-0596
CURRENT APPLICATION NUMBER: US/09/925,139
CURRENT FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-48

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCGTGGTGGAGTTGGGTT 82
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGCGTGGTGGAGTTGGGTT 1

RESULT 8

US-09-925-139-49/c
Sequence 49, Application US/09925139
Publication No. US20030092647A1
GENERAL INFORMATION:

APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
APPLICANT: Pam Nero
APPLICANT: Edward Wanciewicz

TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
FILE REFERENCE: ISPH-0596
CURRENT APPLICATION NUMBER: US/09/925,139
CURRENT FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-49

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 GGAGTACGAGATGGAGATT 103


```
Db      20  GGAGTACGGAGATGGAGATT 1
|||||
RESULT 9
US-09-925-139-50/c
; Sequence 50, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Pam Nero
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925.139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-50

Query Match      14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy      120  CTATCCTAAAGGCCCACTGG 139
|||||
Db      20  CTATCCTAAAGGCCCACTGG 1

RESULT 10
US-09-941-094A-1
; Sequence 1, Application US/09941094A
; Patent No. US20020065226A1
; GENERAL INFORMATION:
; APPLICANT: Siler-Khodr, Theresa M.
; TITLE OF INVENTION: NO. US20020065226A1-Mammalian GnRH Analogs and Uses Thereof in Re
; FILE REFERENCE: P7345.2(CIP)
; CURRENT APPLICATION NUMBER: US/09/941,094A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 09/419,161
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Gallus gallus
US-09-941-094A-1

Query Match      12.1%; Score 16.8; DB 9; Length 30;
Best Local Similarity 75.0%; Pred. No. 2.9e+04; Indels 7;
Matches 21; Conservative 0; Mismatches 7; Gaps 0;

Qy      25  AGCACCAGGCTCAGCTGGAACCTGG 52
|||||
Db      2  AGCACTGGTCCCATGGCTGTACCTGG 29

RESULT 11
US-09-865-866-13/c
; Sequence 13, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
```

```
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865.866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-865-866-13

Query Match      11.8%; Score 16.4; DB 11; Length 30;
Best Local Similarity 76.9%; Pred. No. 3.9e+04; Indels 6;
Matches 20; Conservative 0; Mismatches 6; Gaps 0;

Qy      87  GTACGGAGATGGAGATTGGCTCCCAA 112
|||||
Db      28  GTACGAGAGAGGAGCTTGGATGCCAA 3

RESULT 12
US-10-098-263B-25768
; Sequence 25768, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25768
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-25768

Query Match      11.1%; Score 15.4; DB 14; Length 25;
Best Local Similarity 94.1%; Pred. No. 8.5e+04; Indels 1;
Matches 16; Conservative 0; Mismatches 1; Gaps 0;

Qy      86  AGTACGGAGATGGAGAT 102
|||||
Db      2  AGTACTGAGATGGAGAT 18

RESULT 13
US-10-098-263B-15079
; Sequence 15079, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 15079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-15079

Query Match      10.9%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+05; Indels 3;
Matches 17; Conservative 0; Mismatches 0; Gaps 0;
```

QY 43 GGAACCCCTGGTGTCTCTCC 62
DB 5 GGAACCCCTGGTGTCTCAGGTCC 24

RESULT 14

US-09-908-130-18
; Sequence 18, Application US/09908130
; Patent No. US20020051992A1

; GENERAL INFORMATION:

```

; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Brenner, Sydney
; APPLICANT: Pallas, Michael C.
; TITLE OF INVENTION: System and Apparatus for Sequential
; FILE REFERENCE: 5525-0035.22
; CURRENT APPLICATION NUMBER: US/09/908,130
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

;
; OTHER INFORMATION: synthetic encoded adaptor
; NAME/KEY: misc_feature
; LOCATION: (1) ... (4)

```

OTHER INFORMATION: n = A, T, C or G
US-09-908-130-18

Query Match 10.9%; Score 15.2; DB 9; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels

Qy .
db

RESULT 15

US-09-908-131-18
; Sequence 18, Application US/09908131
; Patent No. US20020061529A1

GENERAL INFORMATION:

APPLICANT: Bridgham, John
 APPLICANT: Corcoran, Kevin P.
 APPLICANT: Golda, George S.
 APPLICANT: Brenner, Sydney
 APPLICANT: Pallas, Michael C.
 TITLE OF INVENTION: System and Apparatus for Sequential
 TITLE OF INVENTION: Processing of Analytes
 FILE REFERENCE: 5525-0035-21
 CURRENT APPLICATION NUMBER: US/09/908,131
 CURRENT FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: US 09/424,028
 PRIOR FILING DATE: 1999-11-16
 PRIOR APPLICATION NUMBER: PCT/US98/11224
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: US 08/862,610
 PRIOR FILING DATE: 1997-05-23
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 18

```

; LENGTH: 30
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFO:
; NAME/KEY:
; LOCATION:

```

Query Match 10.9%; Score 15.2; DB 9; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels

QY 37 ACAGCTGGAACCCCTGGTGTC 56
|||
Db 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 16

US-09-907-795-18
; Sequence 18, Application US/09907795
; Patent No. US20020137052A1

; GENERAL INFORMATION:

```

: APPLICANT: Bridgham, John
: APPLICANT: Corcoran, Kevin P.
: APPLICANT: Goida, George S.
: APPLICANT: Brenner, Sydney
: APPLICANT: Pallas, Michael C.
: TITLE OF INVENTION: System and Apparatus for Sequential
: TITLE OF INVENTION: Processing of Analyses
: FILE REFERENCE: 5525-0035.23
: CURRENT APPLICATION NUMBER: US/09/907,795
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: US 09/424,028
: PRIOR FILING DATE: 1999-11-16
: PRIOR APPLICATION NUMBER: PCT/US98/11224
: PRIOR FILING DATE: 1998-05-22
: PRIOR APPLICATION NUMBER: US 08/862,610
: PRIOR FILING DATE: 1997-05-23
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 18

```

LENGTH: 30
TYPE: DNA
ORGANISM: A

```

; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; NAME/KEY: misc_feature
; LOCATION: (1)...(4)

```

OTHER INFORMATION: n = A, T, C or G
US-09-907-795-18

Query Match 10.9%; Score 15.2; DB 10; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels

QY 37- ACAGCTGGAACCCCTGGTGTC 56
|||||
db 6 ACAGCTGCATCCCCTGGTGAC 25

RESULT 17

US-10-124-884-18
; Sequence 18, Application US/10124884
; Publication No. US20030077615A1
; GENERAL INFORMATION:
; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Pallas, Michael C.
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: Planar Arrays of

```
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: 5525-8035:US05
; CURRENT APPLICATION NUMBER: US/10/124,884
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-10-124-884-18

Query Match      10.9%; Score 15.2; DB 14; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGAAACCTCGTGTC 56
      ||||| ||||| ||||| |||||
DB 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 18
US-10-098-263B-4644/c
; Sequence 4644, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 4644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-4644

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 AAGTTGGGTTAGGAGTACGAGA 95
      ||||| ||||| ||||| |||||
DB 24 AAGTTCGGTGAGGAGTCCGTAGA 2

RESULT 19
US-10-098-263B-108698
; Sequence 108698, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121355/c
; Sequence 121355, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121355

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 TCCTCCAGCGTGTC 71
      ||||| ||||| ||||| |||||
```

```
Db      25  TCCTCCACCGTGGTG 11

RESULT 22
US-09-923-246-31/c
; Sequence 31, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19932
US-09-923-246-31

Query Match      10.8%; Score 15; DB 10; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      40  GCTGGAACCTGTGTCTCTCTCC 62
          |||||
Db      24  GCTGGAACCTCACGGATCTCTCC 2

RESULT 23
US-09-825-561A-22/c
; Sequence 22, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19932
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US-09-825-561A-22

OTHER INFORMATION: Oligonucleotide primer ZC19932

Query Match      10.8%; Score 15; DB 10; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      40  GCTGGAACCTGTGTCTCTCTCC 62
          |||||
Db      24  GCTGGAACCTCACGGATCTCTCC 2

RESULT 24
US-10-243-072-43/c
; Sequence 43, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Bartell C.
; APPLICANT: No. US20030148447A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHALL
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19932
US-10-243-072-43

Query Match      10.8%; Score 15; DB 12; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      40  GCTGGAACCTGTGTCTCTCTCC 62
          |||||
Db      24  GCTGGAACCTCACGGATCTCTCC 2

RESULT 25
US-10-295-723-31/c
; Sequence 31, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
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; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19932
US-10-295-723-31

Query Match      10.8%; Score 15; DB 14; Length 29;
Best Local Similarity 78.3%; Pred.No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      40 GCTGGAACCCCTGGTCTCCTCC 62
        |||||
Db      24 GCTGGAACCCCTACCGATCCTCC 2

Search completed: August 22, 2003, 11:06:14
Job time : 168 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 09:57:54 ; Search time 1611 Seconds
(without alignments)
2097.034 Million cell updates/sec

Title: US-09-925-139-3_COPY_1631_1769

Perfect score: 139

Sequence: 1 ggaatggggctttagcagaa.....ctatcctaagagccactgg 139

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hic.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15	10.8	27	AZ330939	AZ330939 IM0056E11
C 3	14.6	10.5	24	AZ861819	AZ861819 2M0168L12
C 4	14.6	10.5	25	AZ453525	AZ453525 IM0255A01

C 78	12.2	8.8	29	AZ795012	2M0049104	151	11.6	8.3	28	AZ438215	AZ438215	1M0228K12
C 79	12.2	8.8	30	BE384733	601277335	152	11.6	8.3	28	AZ463404	AZ463404	1M0272011
C 80	12.2	8.8	30	AZ584820	1M0389A14	153	11.6	8.3	28	AZ784264	AZ784264	2M0026120
C 81	12	8.6	22	AI444134	FB44801.Y	154	11.6	8.3	28	AZ792783	AZ792783	2M0045C01
C 82	12	8.6	22	TA376G03Q		155	11.6	8.3	28	BH810422	BH810422	SALK_0495
C 83	12	8.6	23	AZ455732	2M0258B16	156	11.6	8.3	29	AZ346074	AZ346074	1M0081105
C 84	12	8.6	25	AG263801	Lotus jap	157	11.6	8.3	29	AZ503753	AZ503753	1M0343H09
C 85	12	8.6	26	TA127E06P	AL462767 T. brucei	158	11.6	8.3	29	AZ666737	AZ666737	1M0549006
C 86	12	8.6	27	AU255344	AU255344	159	11.6	8.3	29	BZ379180	BZ379180	SALK_1129
C 87	12	8.6	27	AZ465524	AZ465524	160	11.6	8.3	30	BE274322	BE274322	601121015
C 88	12	8.6	27	AZ783077	2M0024A01	161	11.6	8.3	30	BE280898	BE280898	601155490
C 89	12	8.6	27	AZ817236	2M0086D03	162	11.6	8.3	30	AZ474193	AZ474193	1M0290J02
C 90	12	8.6	27	AZ836891	2M0131N22	163	11.6	8.3	30	BH866519	BH866519	SALK_1014
C 91	12	8.6	27	AZ840204	2M0136H08	164	11.6	8.3	30	AJ303573	AJ303573	Plasmid
C 92	12	8.6	28	AJ919484	AJ919484 v220f02.r	165	11.4	8.2	17	BM395359	BM395359	50072-2-8
C 93	12	8.6	28	AZ317107	1M0035E09	166	11.4	8.2	20	AZ359918	AZ359918	1M0103A01
C 94	12	8.6	28	AZ737089	1M0584J23	167	11.4	8.2	21	AZ443821	AZ443821	1M0238107
C 95	12	8.6	29	AU258028	AU258028	168	11.4	8.2	22	AI677768	AI677768	WC80B01.X
C 96	12	8.6	29	N27011	N27011 yw73b09.s1	169	11.4	8.2	22	AI748552	AI748552	sb54f11.Y
C 97	12	8.6	29	CC179015	SALK_0570	170	11.4	8.2	22	AI748552	AI748552	sb54f11.Y
C 98	12	8.6	29	BH418365	eco-E1 Mu	171	11.4	8.2	22	AU259732	AU259732	AU259732
C 99	12	8.6	30	AZ666649	1M0548M19	172	11.4	8.2	22	AZ608971	AZ608971	1M0433D04
C 100	11.8	8.5	22	AZ666649	1M0548M19	173	11.4	8.2	23	AZ305600	AZ305600	1M0006A19
C 101	11.8	8.5	24	AZ819297	2M0038L17	174	11.4	8.2	23	BH857265	BH857265	SALK_0765
C 102	11.8	8.5	24	AZ819297	2M0038L17	175	11.4	8.2	23	TA130F01Q	TA130F01Q	T. brucei
C 103	11.8	8.5	24	AZ819297	2M0038L17	176	11.4	8.2	24	AZ601725	AZ601725	1M0420E12
C 104	11.8	8.5	25	TA84A06P	AL462065 T. brucei	177	11.4	8.2	24	AZ663558	AZ663558	1M0543E13
C 105	11.8	8.5	26	AZ782918	2M0024L10	178	11.4	8.2	24	AZ800048	AZ800048	2M0057C24
C 106	11.8	8.5	26	AZ782918	2M0024L10	179	11.4	8.2	24	AZ831249	AZ831249	2M0110G21
C 107	11.8	8.5	27	AZ416143	H84968 y898C08.r1	180	11.4	8.2	25	AI000890	AI000890	0856H04.s
C 108	11.8	8.5	27	AZ623078	1M0460G19	181	11.4	8.2	25	AI586975	AI586975	tw15G05.X
C 109	11.8	8.5	27	AZ623078	1M0460G19	182	11.4	8.2	25	AZ303792	AZ303792	1M0003H07
C 110	11.8	8.5	28	AU270595	AU270595	183	11.4	8.2	25	AZ565950	AZ565950	1M0532M15
C 111	11.8	8.5	28	CO0171	HUMGS000582	184	11.4	8.2	25	BH789422	BH789422	SALK_0293
C 112	11.8	8.5	28	AZ623636	1M0461N05	185	11.4	8.2	27	AZ482018	AZ482018	1M0394H09
C 113	11.8	8.5	28	AZ776516	2M0010K24	186	11.4	8.2	27	AZ586887	AZ586887	1M0394H09
C 114	11.8	8.5	28	AZ776516	2M0010K24	187	11.4	8.2	28	AI119990	AI119990	uc25c01.r
C 115	11.8	8.5	29	AZ776516	2M0010K24	188	11.4	8.2	28	AI156146	AI156146	ue08F05.r
C 116	11.8	8.5	30	BZ276866	601178428	189	11.4	8.2	28	AI537875	AI537875	tp32F04.X
C 117	11.8	8.5	30	BZ276866	601178428	190	11.4	8.2	28	AI930845	AI930845	8B4301.Y
C 118	11.8	8.5	30	BZ276866	601178428	191	11.4	8.2	28	AZ5850025	AZ5850025	2M0151P07
C 119	11.8	8.5	30	AZ230072	Lotus jap	192	11.4	8.2	28	AJ546620	AJ546620	Drosophila
C 120	11.8	8.5	30	DR19J3S	AL736211 Danilo rer	193	11.4	8.2	28	AL477877	AL477877	T. brucei
C 121	11.6	8.3	19	AZ777470	2M0011H21	194	11.4	8.2	28	AZ419519	AZ419519	1M0196N03
C 122	11.6	8.3	20	AZ308311	1M0011J12	195	11.4	8.2	28	AZ651322	AZ651322	1M0521P20
C 123	11.6	8.3	20	AZ331568	1M0059N03	196	11.4	8.2	29	AZ794050	AZ794050	2M0047H09
C 124	11.6	8.3	21	AZ378432	2M0254G15	197	11.4	8.2	29	AZ817122	AZ817122	2M0086C16
C 125	11.6	8.3	22	BG925518	HNC5-1-C1	198	11.4	8.2	29	BZ377903	BZ377903	SALK_1063
C 126	11.6	8.3	22	BG925518	HNC5-1-E	199	11.4	8.2	29	TA211B01P	TA211B01P	T. brucei
C 127	11.6	8.3	22	BG925518	HNC5-1-E	200	11.4	8.2	30	AU259645	AU259645	AU259645
C 128	11.6	8.3	22	BQ584930	E011828-0	201	11.4	8.2	30	BE883323	BE883323	601509063
C 129	11.6	8.3	22	AZ966411	2M0236E22	202	11.4	8.2	30	BM393328	BM393328	50071-2-9
C 130	11.6	8.3	22	AZ966411	2M0236E22	203	11.4	8.2	30	BM395411	BM395411	50072-2-9
C 131	11.6	8.3	23	AZ400856	1M0167N17	204	11.4	8.2	30	AZ337154	AZ337154	1M0067B11
C 132	11.6	8.3	23	AZ971749	2M0245C21	205	11.4	8.2	30	AZ834353	AZ834353	2M0117H02
C 133	11.6	8.3	25	AA912548	Q136C01.s	206	11.4	8.2	30	BZ766396	BZ766396	SALK_1373
C 134	11.6	8.3	25	AZ460726	1M0266010	207	11.4	8.2	30	AL938933	AL938933	Arabidops
C 135	11.6	8.3	26	BM888078	TMT492 Hu	208	11.4	8.2	30	TA164F03Q	TA164F03Q	T. brucei
C 136	11.6	8.3	26	AZ352012	1M0090M13	209	11.2	8.1	18	BM675715	BM675715	TOR602767
C 137	11.6	8.3	26	AZ462630	1M0269F08	210	11.2	8.1	18	AZ320153	AZ320153	1M0040L04
C 138	11.6	8.3	27	AU259022	AU259022	211	11.2	8.1	20	AZ320153	AZ320153	1M0376C18
C 139	11.6	8.3	27	AZ352726	1M0091N13	212	11.2	8.1	20	AZ615402	AZ615402	1M0444A16
C 140	11.6	8.3	27	AZ447932	2M0245013	213	11.2	8.1	20	AZ657958	AZ657958	1M0534802
C 141	11.6	8.3	27	AZ835139	2M0129P09	214	11.2	8.1	21	AZ820567	AZ820567	2M0092B19
C 142	11.6	8.3	27	AZ881096	2M0258120	215	11.2	8.1	21	AZ969578	AZ969578	2M0242G20
C 143	11.6	8.3	28	AA761725	n288g11.s	216	11.2	8.1	22	AI630912	AI630912	tz31903.X
C 144	11.6	8.3	28	AI023489	OV70H01.s	217	11.2	8.1	22	AI650946	AI650946	wa96a02.X
C 145	11.6	8.3	28	AI023489	tz36C05.X	218	11.2	8.1	22	AZ445474	AZ445474	1M0241N14
C 146	11.6	8.3	28	AI783508	N79189 zalld10.r1	219	11.2	8.1	23	AZ800080	AZ800080	2M0057I22
C 147	11.6	8.3	28	N79189		220	11.2	8.1	24	AZ825943	AZ825943	2M0101H19
C 148	11.6	8.3	28	AZ312882	1M0029D05	221	11.2	8.1	24	TA113F01Q	TA113F01Q	T. brucei
C 149	11.6	8.3	28	AZ345524	1M0080M01	222	11.2	8.1	25	AI147073	AI147073	OK33C05.s
C 150	11.6	8.3	28	AZ346701	1M0082K06	223	11.2	8.1	25	AZ774084	AZ774084	2M0003A07

224	11.2	8.1	25	28	AZ937578	2M0195L17	AZ937578	2M0195L17	11	7.9	26	28	AZ357556	1M0099K10
225	11.2	8.1	25	29	TA237D08Q	AL481334 T. brucei	AL481334	T. brucei	11	7.9	26	28	AZ445168	1M0240J13
226	11.2	8.1	26	12	BG900896	HOA7-1-A4	BG900896	HOA7-1-A4	11	7.9	26	28	AZ664004	1M0543O19
227	11.2	8.1	26	28	AZ424207	1M0203N07	AZ424207	1M0203N07	11	7.9	26	28	AZ942099	2M0202C09
228	11.2	8.1	26	28	AZ495519	1M0337P15	AZ495519	1M0337P15	11	7.9	26	29	TA151E04P	AL467331 T. brucei
229	11.2	8.1	26	28	AZ632192	1M0486O12	AZ632192	1M0486O12	11	7.9	27	12	BM400457	5M09-0-73
230	11.2	8.1	27	14	D18734	MUSGS01796	D18734	MUSGS01796	11	7.9	27	28	AZ345323	1M0079M16
231	11.2	8.1	27	28	AZ479687	1M0300H02	AZ479687	1M0300H02	11	7.9	27	28	AZ465567	1M0275C17
232	11.2	8.1	27	28	AZ783050	2M0024J21	AZ783050	2M0024J21	11	7.9	27	28	AZ468814	1M0282G02
233	11.2	8.1	27	28	AZ873243	2M0103N04	AZ873243	2M0103N04	11	7.9	27	28	AZ473031	1M0288I12
234	11.2	8.1	27	28	AZ86947	2M0147P15	AZ86947	2M0147P15	11	7.9	27	28	AZ792850	2M0045B10
235	11.2	8.1	27	28	BH851753	SALK_0734	BH851753	SALK_0734	11	7.9	27	28	AZ792850	2M0045B10
236	11.2	8.1	28	9	A1544609	fb76e03.x	A1544609	fb76e03.x	11	7.9	28	9	A1544609	fb76e03.x
237	11.2	8.1	28	9	AZ633489	1M0109I06	AZ633489	1M0109I06	11	7.9	28	9	A1544609	fb76e03.x
238	11.2	8.1	28	28	AZ403083	1M0170P09	AZ403083	1M0170P09	11	7.9	28	28	A1544609	fb76e03.x
239	11.2	8.1	28	28	AZ650845	1M0521B13	AZ650845	1M0521B13	11	7.9	28	28	A1544609	fb76e03.x
240	11.2	8.1	28	28	AZ790279	2M0338P08	AZ790279	2M0338P08	11	7.9	28	28	A1544609	fb76e03.x
241	11.2	8.1	28	28	AZ941528	2M0201L14	AZ941528	2M0201L14	11	7.9	28	28	A1544609	fb76e03.x
242	11.2	8.1	28	28	BH855787	SALK_0845	BH855787	SALK_0845	11	7.9	28	28	A1544609	fb76e03.x
243	11.2	8.1	28	29	BZ594385	SALK_0840	BZ594385	SALK_0840	11	7.9	28	29	BZ594385	SALK_0840
244	11.2	8.1	29	9	AU258464	AU258464	AU258464	AU258464	11	7.9	29	9	AU258464	AU258464
245	11.2	8.1	29	28	AZ424753	1M0204F04	AZ424753	1M0204F04	11	7.9	29	28	AZ424753	1M0204F04
246	11.2	8.1	29	28	AZ840358	2M0136D22	AZ840358	2M0136D22	11	7.9	29	28	AZ840358	2M0136D22
247	11.2	8.1	29	28	AZ985140	2M0266H20	AZ985140	2M0266H20	11	7.9	29	28	AZ985140	2M0266H20
248	11.2	8.1	29	28	BH907056	SALK_0378	BH907056	SALK_0378	11	7.9	29	28	BH907056	SALK_0378
249	11.2	8.1	29	29	CC457201	SALK_1072	CC457201	SALK_1072	11	7.9	29	29	CC457201	SALK_1072
250	11.2	8.1	29	29	TA263B02P	AL483789 T. brucei	TA263B02P	AL483789 T. brucei	11	7.9	29	29	TA263B02P	AL483789 T. brucei
251	11.2	8.1	30	9	AU244302	AU244302	AU244302	AU244302	11	7.9	30	9	AU244302	AU244302
252	11.2	8.1	30	10	BE277260	601178250	BE277260	601178250	11	7.9	30	10	BE277260	601178250
253	11.2	8.1	30	10	BE295129	601173573	BE295129	601173573	11	7.9	30	10	BE295129	601173573
254	11.2	8.1	30	10	BE295129	601173573	BE295129	601173573	11	7.9	30	10	BE295129	601173573
255	11.2	8.1	30	10	BE378923	601237514	BE378923	601237514	11	7.9	30	10	BE378923	601237514
256	11.2	8.1	30	10	BE559533	601345383	BE559533	601345383	11	7.9	30	10	BE559533	601345383
257	11.2	8.1	30	12	B122858	602941108	B122858	602941108	11	7.9	30	12	B122858	602941108
258	11.2	8.1	30	28	AZ323517	1M0045A04	AZ323517	1M0045A04	11	7.9	30	28	AZ323517	1M0045A04
259	11.2	8.1	30	28	AZ337154	1M0067B11	AZ337154	1M0067B11	11	7.9	30	28	AZ337154	1M0067B11
260	11.2	8.1	30	28	AZ343221	1M0076K02	AZ343221	1M0076K02	11	7.9	30	28	AZ343221	1M0076K02
261	11.2	8.1	30	28	AZ416610	1M0132L06	AZ416610	1M0132L06	11	7.9	30	28	AZ416610	1M0132L06
262	11.2	8.1	30	28	AZ588957	1M0397B08	AZ588957	1M0397B08	11	7.9	30	28	AZ588957	1M0397B08
263	11.2	8.1	30	28	AZ591789	1M0402P06	AZ591789	1M0402P06	11	7.9	30	28	AZ591789	1M0402P06
264	11.2	8.1	30	28	AZ783946	2M0036B08	AZ783946	2M0036B08	11	7.9	30	28	AZ783946	2M0036B08
265	11.2	8.1	30	28	AZ787677	2M0034H17	AZ787677	2M0034H17	11	7.9	30	28	AZ787677	2M0034H17
266	11.2	8.1	30	28	AZ810546	2M0076F10	AZ810546	2M0076F10	11	7.9	30	28	AZ810546	2M0076F10
267	11.2	8.1	30	28	AZ824893	2M0099H17	AZ824893	2M0099H17	11	7.9	30	28	AZ824893	2M0099H17
268	11.2	8.1	30	28	AZ827938	2M0104J09	AZ827938	2M0104J09	11	7.9	30	28	AZ827938	2M0104J09
269	11.2	8.1	30	28	AZ795136	2M0049A16	AZ795136	2M0049A16	11	7.9	30	28	AZ795136	2M0049A16
270	11.2	8.1	30	28	AZ445379	1M0241E07	AZ445379	1M0241E07	11	7.9	30	28	AZ445379	1M0241E07
271	11.2	8.1	30	28	AZ811106	2M0077P03	AZ811106	2M0077P03	11	7.9	30	28	AZ811106	2M0077P03
272	11.2	8.1	30	28	AZ509602	1M0352E08	AZ509602	1M0352E08	11	7.9	30	28	AZ509602	1M0352E08
273	11.2	8.1	30	28	A139277	t154a02.x	A139277	t154a02.x	11	7.9	30	28	A139277	t154a02.x
274	11.2	8.1	30	28	AZ478594	1M0298H15	AZ478594	1M0298H15	11	7.9	30	28	AZ478594	1M0298H15
275	11.2	8.1	30	28	AZ640656	1M0502K14	AZ640656	1M0502K14	11	7.9	30	28	AZ640656	1M0502K14
276	11.2	8.1	30	28	AZ779122	2M0015M03	AZ779122	2M0015M03	11	7.9	30	28	AZ779122	2M0015M03
277	11.2	8.1	30	28	AZ787955	2M0034E18	AZ787955	2M0034E18	11	7.9	30	28	AZ787955	2M0034E18
278	11.2	8.1	30	28	AZ829662	2M0263J06	AZ829662	2M0263J06	11	7.9	30	28	AZ829662	2M0263J06
279	11.2	8.1	30	28	TA110C02Q	AL461782 T. brucei	TA110C02Q	AL461782 T. brucei	11	7.9	30	28	TA110C02Q	AL461782 T. brucei
280	11.2	8.1	30	28	AZ308569	1M0011M08	AZ308569	1M0011M08	11	7.9	30	28	AZ308569	1M0011M08
281	11.2	8.1	30	28	AZ331549	1M0059K02	AZ331549	1M0059K02	11	7.9	30	28	AZ331549	1M0059K02
282	11.2	8.1	30	28	AZ435508	1M0080I01	AZ435508	1M0080I01	11	7.9	30	28	AZ435508	1M0080I01
283	11.2	8.1	30	28	AZ470241	1M0284B16	AZ470241	1M0284B16	11	7.9	30	28	AZ470241	1M0284B16
284	11.2	8.1	30	28	AZ627985	1M0476O06	AZ627985	1M0476O06	11	7.9	30	28	AZ627985	1M0476O06
285	11.2	8.1	30	28	AZ785457	2M0039A24	AZ785457	2M0039A24	11	7.9	30	28	AZ785457	2M0039A24
286	11.2	8.1	30	28	AZ785926	2M0030K08	AZ785926	2M0030K08	11	7.9	30	28	AZ785926	2M0030K08
287	11.2	8.1	30	28	AZ970753	2M0244E01	AZ970753	2M0244E01	11	7.9	30	28	AZ970753	2M0244E01
288	11.2	8.1	30	28	AZ449706	1M0248M02	AZ449706	1M0248M02	11	7.9	30	28	AZ449706	1M0248M02
289	11.2	8.1	30	28	AZ455814	1M0258B21	AZ455814	1M0258B21	11	7.9	30	28	AZ455814	1M0258B21
290	11.2	8.1	30	28	AZ621109	1M0454D12	AZ621109	1M0454D12	11	7.9	30	28	AZ621109	1M0454D12
291	11.2	8.1	30	28	AZ825943	2M0101H19	AZ825943	2M0101H19	11	7.9	30	28	AZ825943	2M0101H19
292	11.2	8.1	30	28	AZ825943	2M0101H19	AZ825943	2M0101H19	11	7.9	30	28	AZ825943	2M0101H19
293	11.2	8.1	30	28	A1025765	ov94a03.s	A1025765	ov94a03.s	11	7.9	30	28	A1025765	ov94a03.s
294	11.2	8.1	30	28	AZ620092	1M0452J07	AZ620092	1M0452J07	11	7.9	30	28	AZ620092	1M0452J07
295	11.2	8.1	30	28	AZ774118	2M0003K08	AZ774118	2M0003K08	11	7.9	30	28	AZ774118	2M0003K08
296	11.2	8.1	30	28	AZ345607	1M0080C20	AZ345607	1M0080C20	11	7.9	30	28	AZ345607	1M0080C20

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C 370	10.8	7.8	25	9	AI155015	AI155015 ud78a02.r	443	10.6	7.6	19	28	AZ761834	AZ761834
C 371	10.8	7.8	25	9	AI361952	AI361952 QY37E02.x	444	10.6	7.6	20	28	AZ308179	AZ308179
C 372	10.8	7.8	25	9	AI363940	AI363940 QW34B12.x	445	10.6	7.6	20	28	AZ333215	AZ333215
C 373	10.8	7.8	25	12	BI094828	BI094828 EST-CD34N	446	10.6	7.6	20	28	AZ333930	AZ333930
C 374	10.8	7.8	25	12	BI094828	BI094828 5009-0-2-	447	10.6	7.6	20	28	AZ423776	AZ423776
C 375	10.8	7.8	25	14	C00104	C00104 HUNG0000572	448	10.6	7.6	20	28	AZ592780	AZ592780
C 376	10.8	7.8	25	28	AZ584819	AZ584819 LM0389A13	449	10.6	7.6	20	28	AZ601843	AZ601843
C 377	10.8	7.8	25	28	AZ588162	AZ588162 LM0396K07	450	10.6	7.6	20	28	AZ658035	AZ658035
C 378	10.8	7.8	25	28	AZ803224	AZ803224 LM06380A	451	10.6	7.6	20	28	AZ833186	AZ833186
C 379	10.8	7.8	25	28	AZ810739	AZ810739 LM0676C02	452	10.6	7.6	20	28	AZ835025	AZ835025
C 380	10.8	7.8	25	28	AZ838825	AZ838825 LM0197005	453	10.6	7.6	20	28	TA158A03P	TA158A03P
C 381	10.8	7.8	25	14	T61018	T61018 Yb74b11.r1	454	10.6	7.6	21	9	AU254493	AU254493
C 382	10.8	7.8	26	28	AZ320242	AZ320242 LM0040M12	455	10.6	7.6	21	28	AZ626594	AZ626594
C 383	10.8	7.8	26	28	AZ449518	AZ449518 LM0247K13	456	10.6	7.6	21	28	AZ758704	AZ758704
C 384	10.8	7.8	26	28	AZ459978	AZ459978 LM0265F07	457	10.6	7.6	22	9	AI183338	AI183338
C 385	10.8	7.8	26	28	AZ779432	AZ779432 LM0015P14	458	10.6	7.6	22	9	AI441822	AI441822
C 386	10.8	7.8	26	28	BZ353740	BZ353740 SALK_1220	459	10.6	7.6	22	14	D21051	D21051
C 387	10.8	7.8	26	29	BZ384018	BZ384018 SALK_1349	460	10.6	7.6	23	28	AZ3339346	AZ3339346
C 388	10.8	7.8	26	29	BM396690	BM396690 5009-0-24	461	10.6	7.6	23	28	AZ416800	AZ416800
C 389	10.8	7.8	27	12	BM396690	BM396690 5009-0-24	462	10.6	7.6	23	28	AZ450507	AZ450507
C 390	10.8	7.8	27	28	AZ418585	AZ418585 LM0194A18	463	10.6	7.6	23	28	AZ822792	AZ822792
C 391	10.8	7.8	27	28	AZ418585	AZ418585 SALK_1031	464	10.6	7.6	23	28	AZ822965	AZ822965
C 392	10.8	7.8	27	29	BZ593155	BZ593155 SALK_0622	465	10.6	7.6	23	28	AZ822965	AZ822965
C 393	10.8	7.8	27	29	AZ226118	AZ226118 Lotus_jap	466	10.6	7.6	23	28	AZ979817	AZ979817
C 394	10.8	7.8	27	29	TA292F02P	TA292F02P	467	10.6	7.6	23	29	TA380G08Q	TA380G08Q
C 395	10.8	7.8	28	9	AI376644	AI376644 te63b01.x	468	10.6	7.6	24	28	AZ623720	AZ623720
C 396	10.8	7.8	28	9	AI522573	AI522573 fb59d12.x	469	10.6	7.6	24	28	AZ658406	AZ658406
C 397	10.8	7.8	28	9	AI677996	AI677996 wc81e09.x	470	10.6	7.6	24	28	AZ800644	AZ800644
C 398	10.8	7.8	28	12	BM393660	BM393660 50072-2-1	471	10.6	7.6	25	9	AA881443	AA881443
C 399	10.8	7.8	28	12	BM393660	BM393660 50071-2-1	472	10.6	7.6	25	9	AA881443	AA881443
C 400	10.8	7.8	28	14	H14469	H14469 YL25H01.r1	473	10.6	7.6	25	12	BG2925523	BG2925523
C 401	10.8	7.8	28	28	AQ026271	AQ026271 1(3)L6241	474	10.6	7.6	25	13	BQ584791	BQ584791
C 402	10.8	7.8	28	28	AZ245558	AZ245558 LM0080M22	475	10.6	7.6	25	13	BQ584791	BQ584791
C 403	10.8	7.8	28	28	AZ480483	AZ480483 LM0302J04	476	10.6	7.6	25	13	BQ589704	BQ589704
C 404	10.8	7.8	28	28	AZ806070	AZ806070 LM0067G21	477	10.6	7.6	25	14	N32966	N32966
C 405	10.8	7.8	28	28	AZ811033	AZ811033 LM0077B02	478	10.6	7.6	25	28	AZ364139	AZ364139
C 406	10.8	7.8	28	28	BM392636	BM392636 50071-2-1	479	10.6	7.6	25	28	AZ776661	AZ776661
C 407	10.8	7.8	28	28	BM392636	BM392636 50071-2-1	480	10.6	7.6	25	28	AZ776661	AZ776661
C 408	10.8	7.8	28	28	BM392636	BM392636 50071-2-1	481	10.6	7.6	25	28	AZ776661	AZ776661
C 409	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	482	10.6	7.6	25	28	AZ776661	AZ776661
C 410	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	483	10.6	7.6	25	28	AZ776661	AZ776661
C 411	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	484	10.6	7.6	25	28	AZ776661	AZ776661
C 412	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	485	10.6	7.6	25	28	AZ776661	AZ776661
C 413	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	486	10.6	7.6	25	28	AZ776661	AZ776661
C 414	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	487	10.6	7.6	25	28	AZ776661	AZ776661
C 415	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	488	10.6	7.6	25	28	AZ776661	AZ776661
C 416	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	489	10.6	7.6	25	28	AZ776661	AZ776661
C 417	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	490	10.6	7.6	25	28	AZ776661	AZ776661
C 418	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	491	10.6	7.6	25	28	AZ776661	AZ776661
C 419	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	492	10.6	7.6	25	28	AZ776661	AZ776661
C 420	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	493	10.6	7.6	25	28	AZ776661	AZ776661
C 421	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	494	10.6	7.6	25	28	AZ776661	AZ776661
C 422	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	495	10.6	7.6	25	28	AZ776661	AZ776661
C 423	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	496	10.6	7.6	25	28	AZ776661	AZ776661
C 424	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	497	10.6	7.6	25	28	AZ776661	AZ776661
C 425	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	498	10.6	7.6	25	28	AZ776661	AZ776661
C 426	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	499	10.6	7.6	25	28	AZ776661	AZ776661
C 427	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	500	10.6	7.6	25	28	AZ776661	AZ776661
C 428	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	501	10.6	7.6	25	28	AZ776661	AZ776661
C 429	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	502	10.6	7.6	25	28	AZ776661	AZ776661
C 430	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	503	10.6	7.6	25	28	AZ776661	AZ776661
C 431	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	504	10.6	7.6	25	28	AZ776661	AZ776661
C 432	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	505	10.6	7.6	25	28	AZ776661	AZ776661
C 433	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	506	10.6	7.6	25	28	AZ776661	AZ776661
C 434	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	507	10.6	7.6	25	28	AZ776661	AZ776661
C 435	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	508	10.6	7.6	25	28	AZ776661	AZ776661
C 436	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	509	10.6	7.6	25	28	AZ776661	AZ776661
C 437	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	510	10.6	7.6	25	28	AZ776661	AZ776661
C 438	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	511	10.6	7.6	25	28	AZ776661	AZ776661
C 439	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	512	10.6	7.6	25	28	AZ776661	AZ776661
C 440	10.8	7.8	28	28	BM393364	BM393364 50071-2-1	513	10.6	7.6	25	28	AZ776661	AZ776661
C 441	10.6	7.6	19	28	AZ307462	AZ307462 LM0009J08	514	10.6	7.6	28	28	AZ489682	AZ489682
C 442	10.6	7.6	19	28	AZ346707	AZ346707 LM0082M04	515	10.6	7.6	28	28	AZ511067	AZ511067

C 516	10.6	7.6	28	28	AZ512393	1M0357F20	589	10.4	7.5	24	28	AZ505513	1M0346B13
C 517	10.6	7.6	28	28	AZ590898	1M0400A16	590	10.4	7.5	24	28	AZ761059	1M0555L08
C 518	10.6	7.6	28	28	AZ836785	2M0131I14	C 591	10.4	7.5	24	28	AZ796057	2M0051B13
C 519	10.6	7.6	28	28	AZ842146	2M0140D04	C 592	10.4	7.5	24	28	AZ817421	2M0086L12
C 520	10.6	7.6	28	28	AZ974910	2M0249E15	C 593	10.4	7.5	24	28	AZ983288	2M0264G23
C 521	10.6	7.6	28	28	AZ246945	2822529.5	C 594	10.4	7.5	24	28	AZ949806Q	T. brucei
C 522	10.6	7.6	28	28	BM395134	50072-2-7	C 595	10.4	7.5	25	9	AU254124	AU254124
C 523	10.6	7.6	28	28	AZ307046	1M0008E24	C 596	10.4	7.5	25	12	BM395408	50072-2-8
C 524	10.6	7.6	28	28	AZ331636	1M0059O09	C 597	10.4	7.5	25	12	BM396165	5009-0-18
C 525	10.6	7.6	28	28	AZ345862	1M0080I14	C 598	10.4	7.5	25	28	AZ483610	1M0309N21
C 526	10.6	7.6	28	28	AZ398458	1M0163D21	C 599	10.4	7.5	25	28	AZ483610	1M0355F11
C 527	10.6	7.6	28	28	AZ427756	1M0209O20	C 600	10.4	7.5	25	28	AZ510562	1M0355A04
C 528	10.6	7.6	28	28	AZ430267	1M0214K11	C 601	10.4	7.5	25	28	AZ513486	1M0359A04
C 529	10.6	7.6	28	28	AZ432529	1M0218C04	C 602	10.4	7.5	25	28	AZ588253	1M0396O23
C 530	10.6	7.6	28	28	AZ642459	1M0505D06	C 603	10.4	7.5	25	28	AZ621312	1M0454F19
C 531	10.6	7.6	28	28	AZ780387	2M0017N12	C 604	10.4	7.5	25	28	AZ820085	2M0092O01
C 532	10.6	7.6	28	28	AZ815922	2M0084L06	C 605	10.4	7.5	25	28	AZ834056	2M0116L04
C 533	10.6	7.6	28	28	AZ820565	2M0092A22	C 606	10.4	7.5	25	28	AZ943422	2M0204P06
C 534	10.6	7.6	28	28	AZ828807	2M0106J03	C 607	10.4	7.5	25	28	BH405074	KG05441-5
C 535	10.6	7.6	28	28	AZ998267	2M0285D12	C 608	10.4	7.5	25	28	BH863402	SALK_0398
C 536	10.6	7.6	30	14	C01081	HUMGS000773	C 609	10.4	7.5	25	28	BH865143	SALK_0974
C 537	10.6	7.6	30	14	C01081	HUMGS000773	C 610	10.4	7.5	25	29	BZ381299	SALK_1165
C 538	10.6	7.6	30	28	AZ408639	1M0179I23	C 611	10.4	7.5	25	29	TA111D05P	AL461854 T. brucei
C 539	10.6	7.6	30	28	AZ408639	1M0179I23	C 612	10.4	7.5	25	29	TA263P03Q	AL461854 T. brucei
C 540	10.6	7.6	30	28	AZ597778	1M0367I16	C 613	10.4	7.5	26	28	AZ352806Q	AL461854 T. brucei
C 541	10.6	7.6	30	28	AZ587961	1M0336B06	C 614	10.4	7.5	26	28	AZ309024	AL461854 T. brucei
C 542	10.6	7.6	30	28	AZ657672	1M0534G02	C 615	10.4	7.5	26	28	AZ333183	AL461854 T. brucei
C 543	10.6	7.6	30	28	AZ658443	1M0535F23	C 616	10.4	7.5	26	28	AZ783529	AL461854 T. brucei
C 544	10.6	7.6	30	28	AZ783604	2M0025F05	C 617	10.4	7.5	26	28	AZ864944	AL461854 T. brucei
C 545	10.6	7.6	30	28	AZ801555	2M0060M01	C 618	10.4	7.5	26	28	AZ969979	AL461854 T. brucei
C 546	10.6	7.6	30	28	AZ941284	2M0201A02	C 619	10.4	7.5	26	28	BH863961	AL461854 T. brucei
C 547	10.6	7.6	30	28	BH850114	SALK_0708	C 620	10.4	7.5	26	28	CC060543	AL461854 T. brucei
C 548	10.6	7.6	30	28	BZ355049	SALK_1262	C 621	10.4	7.5	26	28	AZ355810	AL461854 T. brucei
C 549	10.6	7.6	30	29	AZ230564	Lotus_jap	C 622	10.4	7.5	27	28	AZ357559	AL461854 T. brucei
C 550	10.6	7.6	30	29	DR31G1T	AL976750 Danio rer	C 623	10.4	7.5	27	28	AZ495213	AL461854 T. brucei
C 551	10.4	7.5	20	13	BQ395025	E012395-0	C 624	10.4	7.5	27	28	AZ594886	AL461854 T. brucei
C 552	10.4	7.5	20	13	BQ395025	E012395-0	C 625	10.4	7.5	27	28	AZ594886	AL461854 T. brucei
C 553	10.4	7.5	20	28	AZ345442	1M0080G08	C 626	10.4	7.5	27	28	AZ813093	AL461854 T. brucei
C 554	10.4	7.5	20	28	AZ393773	1M0157B04	C 627	10.4	7.5	28	9	AA902937	AL461854 T. brucei
C 555	10.4	7.5	20	28	AZ827586	1M02104C08	C 628	10.4	7.5	28	9	AA937308	AL461854 T. brucei
C 556	10.4	7.5	21	12	BG969606	HOA59-1-A	C 629	10.4	7.5	28	9	AI006239	AL461854 T. brucei
C 557	10.4	7.5	21	12	BG969606	HOA59-1-A	C 630	10.4	7.5	28	9	AI019322	AL461854 T. brucei
C 558	10.4	7.5	21	28	AZ348213	1M0084N15	C 631	10.4	7.5	28	9	AI153397	AL461854 T. brucei
C 559	10.4	7.5	21	28	AZ359241	1M0102D03	C 632	10.4	7.5	28	9	AI153397	AL461854 T. brucei
C 560	10.4	7.5	21	28	AZ430565	1M0215A08	C 633	10.4	7.5	28	9	AI686757	AL461854 T. brucei
C 561	10.4	7.5	21	28	AZ442098	1M0234F12	C 634	10.4	7.5	28	13	BQ593191	AL461854 T. brucei
C 562	10.4	7.5	21	28	AZ445481	1M0241P15	C 635	10.4	7.5	28	28	AQ025041	AL461854 T. brucei
C 563	10.4	7.5	21	28	AZ595699	1M0408C02	C 636	10.4	7.5	28	28	AZ309062	AL461854 T. brucei
C 564	10.4	7.5	21	28	AZ610251	1M0435M21	C 637	10.4	7.5	28	28	AZ619085	AL461854 T. brucei
C 565	10.4	7.5	21	28	AZ783428	2M0025F10	C 638	10.4	7.5	28	28	AZ632301	AL461854 T. brucei
C 566	10.4	7.5	21	28	AZ817003	2M0086C04	C 639	10.4	7.5	28	28	AZ811033	AL461854 T. brucei
C 567	10.4	7.5	22	28	AZ334102	1M0063B16	C 640	10.4	7.5	28	28	AZ839856	AL461854 T. brucei
C 568	10.4	7.5	22	28	AZ430045	1M0214O17	C 641	10.4	7.5	28	28	AZ853595	AL461854 T. brucei
C 569	10.4	7.5	22	28	AZ479083	1M0299F03	C 642	10.4	7.5	28	28	BH855787	AL461854 T. brucei
C 570	10.4	7.5	22	28	AZ579287	1M0363K11	C 643	10.4	7.5	28	29	BZ291486	AL461854 T. brucei
C 571	10.4	7.5	22	28	AZ612552	1M0439G12	C 644	10.4	7.5	28	29	BZ664334	AL461854 T. brucei
C 572	10.4	7.5	22	28	AZ631537	1M0485F17	C 645	10.4	7.5	29	14	R31895	AL461854 T. brucei
C 573	10.4	7.5	22	28	AZ711198	1M0573M08	C 646	10.4	7.5	29	28	AZ580321	AL461854 T. brucei
C 574	10.4	7.5	22	28	AZ813877	2M0081P13	C 647	10.4	7.5	29	28	AZ769743	AL461854 T. brucei
C 575	10.4	7.5	23	10	BG668141	DRABWE02	C 648	10.4	7.5	29	28	AZ771858	AL461854 T. brucei
C 576	10.4	7.5	23	28	AZ334719	1M0064P07	C 649	10.4	7.5	29	28	AZ788256	AL461854 T. brucei
C 577	10.4	7.5	23	28	AZ374746	1M0127D15	C 650	10.4	7.5	29	28	AZ834401	AL461854 T. brucei
C 578	10.4	7.5	23	28	AZ387189	1M0146L24	C 651	10.4	7.5	29	28	BH848482	AL461854 T. brucei
C 579	10.4	7.5	23	28	AZ480676	2M0302F23	C 652	10.4	7.5	29	28	BH856361	AL461854 T. brucei
C 580	10.4	7.5	23	28	AZ610143	1M0435H17	C 653	10.4	7.5	29	29	CC057376	AL461854 T. brucei
C 581	10.4	7.5	23	28	AZ610186	1M0435A21	C 654	10.4	7.5	29	29	TA225F03P	AL461854 T. brucei
C 582	10.4	7.5	23	28	AZ646716	1M0512D23	C 655	10.4	7.5	30	2	HS007697	AL461854 T. brucei
C 583	10.4	7.5	23	28	AZ663880	2M0543D14	C 656	10.4	7.5	30	10	BE279576	AL461854 T. brucei
C 584	10.4	7.5	23	28	AZ784963	2M0028F20	C 657	10.4	7.5	30	10	BE384678	AL461854 T. brucei
C 585	10.4	7.5	23	28	AZ863841	2M0173F09	C 658	10.4	7.5	30	10	BE729410	AL461854 T. brucei
C 586	10.4	7.5	24	14	D18741	MUSGS01803	C 659	10.4	7.5	30	12	BI463777	AL461854 T. brucei
C 587	10.4	7.5	24	28	AZ404465	1M0172P09	C 660	10.4	7.5	30	12	BI521544	AL461854 T. brucei
C 588	10.4	7.5	24	28	AZ437306	1M0225D03	C 661	10.4	7.5	30	14	U41135	AL461854 T. brucei

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C 670	10.4	7.5	30	28	AZ472912	1M0288O20	C 743	10.2	7.3	25	28	AG361847	AG361847 Lotu8_jap
C 671	10.4	7.5	30	28	AZ472912	1M0288O20	C 744	10.2	7.3	25	28	AL458440	AL458440 T. brucei
C 672	10.4	7.5	30	28	AZ783172	2M0024F08	C 745	10.2	7.3	26	12	BM398746	BM398746 5009-0-49
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C 675	10.4	7.5	30	28	BH851910	SALK_0736	C 748	10.2	7.3	26	28	AZ617581	AZ617581 1M0448L20
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C 679	10.4	7.5	30	28	AL935924	Arabidops	C 752	10.2	7.3	26	28	AZ769214	AZ769214 1M0558F03
C 680	10.4	7.5	30	28	BX293115	Arabidops	C 753	10.2	7.3	26	28	AZ827167	AZ827167 2M0103N22
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C 683	10.2	7.3	19	28	AZ443948	1M0238F04	C 756	10.2	7.3	26	28	AZ946833	AZ946833 2M0208L15
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C 685	10.2	7.3	19	28	AZ610584	1M0433P20	C 758	10.2	7.3	26	28	AZ955924	AZ955924 2M0222P10
C 686	10.2	7.3	19	28	AZ614760	1M0443A17	C 759	10.2	7.3	26	28	BZ382980	BZ382980 SALK_1192
C 687	10.2	7.3	20	28	AZ307491	1M0009C13	C 760	10.2	7.3	26	28	BZ383240	BZ383240 SALK_1253
C 688	10.2	7.3	20	28	AZ389565	1M0150C24	C 761	10.2	7.3	26	28	CC060543	CC060543 EY04476-3
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C 690	10.2	7.3	20	28	AZ436762	1M0224G12	C 763	10.2	7.3	26	28	AA713615	AA713615 nv70h08.s
C 691	10.2	7.3	20	28	AZ492477	1M0326D11	C 764	10.2	7.3	27	14	H49153	H49153 yq18c01.r1
C 692	10.2	7.3	20	28	AZ802218	2M0060J19	C 765	10.2	7.3	27	14	H77342	H77342 yul12a10.s1
C 693	10.2	7.3	20	28	AZ846316	2M0146N24	C 766	10.2	7.3	27	28	AZ473597	AZ473597 1M0289L04
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C 695	10.2	7.3	20	28	AZ867169	2M0177I20	C 768	10.2	7.3	27	28	AZ506426	AZ506426 1M0347M04
C 696	10.2	7.3	20	28	AZ872579	1M0287F21	C 769	10.2	7.3	27	28	AZ590063	AZ590063 1M0399M24
C 697	10.2	7.3	21	28	AZ512534	1M0358B07	C 770	10.2	7.3	27	28	AZ619590	AZ619590 1M0451H24
C 698	10.2	7.3	21	28	AZ657958	1M0534B02	C 771	10.2	7.3	27	28	AZ685654	AZ685654 2M0029E13
C 699	10.2	7.3	21	28	AZ810730	2M0076A04	C 772	10.2	7.3	27	28	AZ800963	AZ800963 2M0059C16
C 700	10.2	7.3	21	28	AZ826245	2M0101B21	C 773	10.2	7.3	27	28	AZ803234	AZ803234 2M0063G06
C 701	10.2	7.3	21	28	AZ857948	2M0162M21	C 774	10.2	7.3	27	28	AZ842796	AZ842796 2M0141I20
C 702	10.2	7.3	22	28	AZ641435	1M0503P21	C 775	10.2	7.3	27	28	AZ91201	AZ91201 2M0275G13
C 703	10.2	7.3	22	28	AZ774731	2M0004M18	C 776	10.2	7.3	27	28	BZ768296	BZ768296 SALK_1400
C 704	10.2	7.3	22	28	AZ840226	2M0136L08	C 777	10.2	7.3	27	28	AA713615	AA713615 nv70h08.s
C 705	10.2	7.3	22	28	AZ868780	2M0180B12	C 778	10.2	7.3	28	9	AA864650	AA864650 ch37b09.s
C 706	10.2	7.3	22	28	AZ345636	1M0080I19	C 779	10.2	7.3	28	9	AA902937	AA902937 ok43g03.s
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C 708	10.2	7.3	23	28	AZ584523	1M0389C10	C 781	10.2	7.3	28	9	AA153771	AA153771 ud8h01.r
C 709	10.2	7.3	23	28	AZ585214	1M0390C14	C 782	10.2	7.3	28	9	AA1288386	AA1288386 qv85c01.x
C 710	10.2	7.3	23	28	AZ609364	1M0434004	C 783	10.2	7.3	28	9	AA117763	AA117763 mo65d08.r
C 711	10.2	7.3	23	28	AZ782947	2M0024B17	C 784	10.2	7.3	28	9	AA117763	AA117763 mo65d08.r
C 712	10.2	7.3	23	28	AZ783944	2M0026F06	C 785	10.2	7.3	28	9	AA16657	AA16657 sa10b04.x
C 713	10.2	7.3	23	28	AL462961 T. brucei	AL462961 T. brucei	C 786	10.2	7.3	28	9	AA1687005	AA1687005 tp81f02.x
C 714	10.2	7.3	23	28	AA248971	2819552.3	C 787	10.2	7.3	28	9	AA1966725	AA1966725 tp81f02.x
C 715	10.2	7.3	24	28	AZ432307	1M0217J09	C 788	10.2	7.3	28	14	H63106	H63106 yr48a04.s1
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C 723	10.2	7.3	25	9	AI624477	AI624477 t668a04.x	C 796	10.2	7.3	28	28	AZ602808	AZ602808 1M0421B16
C 724	10.2	7.3	25	9	AI648460	AI648460 t256b06.x	C 797	10.2	7.3	28	28	AZ641309	AZ641309 1M0503G17
C 725	10.2	7.3	25	12	BM396163	BM396163 5009-0-18	C 798	10.2	7.3	28	28	AZ658386	AZ658386 1M0558K14
C 726	10.2	7.3	25	13	BQ121142	BQ121142 EST606718	C 799	10.2	7.3	28	28	AZ800846	AZ800846 2M0059N05
C 727	10.2	7.3	25	14	CA909996	CA909996 PCSC06235	C 800	10.2	7.3	28	28	AZ834553	AZ834553 2M0117N13
C 728	10.2	7.3	25	14	H93534	H93534 yv08g12.r1	C 801	10.2	7.3	28	28	AZ837343	AZ837343 2M0132M04
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C 730	10.2	7.3	25	28	AZ371108	AZ371108 1M0122I03	C 803	10.2	7.3	28	28	AZ843789	AZ843789 2M0142L15
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C 732	10.2	7.3	25	28	AZ500456	AZ500456 1M0338017	C 805	10.2	7.3	28	28	AZ980190	AZ980190 2M0257G09
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C 875 10.2 7.2 19 12 BM395903
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25 29 BZ381778
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AI664044 ue73e05.r
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BZ381778 SALK_1172
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BZ597082 SALK_0993

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0434 row: P column: 17
Seq primer: CCGTGAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES SOURCE

1. -28

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/db_xref="taxon:10090"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G1_4732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

2-6 10 8 t

BASE COUNT	3 a	7 c	10 g	8 t
ORIGIN				
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Best Local Similarity	86.4%;	Pred. No. 4.1e+05;		
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	Gaps	0;		

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RESULT 2
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LOCUS
DEFINITION AZ330939 linear DNA 27 bp GSS 29-SEP-2000
DEFINITION 1M005681R Mouse 10kb plasmid UUCGIM library Mus musculus genomic cDNA sequence

clone UUGC1M0056E11 K, genomic survey sequence:
 AZ330939
 AZ330939.1 GI:10393139
 VERSION
 GSS.
 KEYWORDS

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 27)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, B., Hamli, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

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C 982	10	7.2	27	12	BF9398876	BF9398876 5009-0-50
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C 995	10	7.2	27	29	BZ380070	BZ380070 SALK 1145
C 996	10	7.2	27	29	TA128C06P	TA128C06P T. brucei
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ALIGNMENTS

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DEFINITION				

ACCESSION AZ609431
VERSION AZ609431.1
KEYWORDS GSS. GI:11731717

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 28) Barber M. Beacorn T. Duval B. Hamil C.

AUTHORS Dunn, D., Aoyagi, A., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly, Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D. Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

CONTACT Robert B. Weiss

JOURNAL COMMENT
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0255 row: A column: 01
 Seq primer: CGTTGTAAACAGCGCCAGT
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 High quality sequence stop: 25.
 Location/Qualifiers
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 7 a 9 c 6 g 3 c
 BASE COUNT
 ORIGIN
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 Best Local Similarity 81.0%; Pred. No. 2.2e+06;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 Db 21 TGGAGTGCCCTCCAGTGTGT 1
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 RESULT 5
 AZ486858/c 28 bp DNA linear GSS 05-OCT-2000
 LOCUS
 DEFINITION
 1M0315H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315H19 R, genomic survey sequence.
 ACCESSION
 AZ486858
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

JOURNAL COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: H column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0315H19"
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 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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 ORIGIN
 Query Match 10.5%; Score 14.6; DB 28; Length 28;
 Best Local Similarity 81.0%; Pred. No. 2.3e+06;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 8 GCTTGTAGCAGAGCGCAAGCA 28
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 Db 21 GTTTGTAGGAGAGCAACCA 1
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 LOCUS
 DEFINITION
 1M0414F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0414F08 F, genomic survey sequence.
 ACCESSION
 AZ599021
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquiqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 1.

FEATURES

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 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP_Prl"
 /note="Vector: PAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
 6 a 6 c 9 g 7 t

BASE COUNT

ORIGIN
 Query Match 10.1%; Score 14; DB 9; Length 28;
 Best Local Similarity 77.3%; Pred. No. 3.4e+06;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 19 AAGCAAGCAGCAGCTCAG 40
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Db 27 ATGCCAAGTACTGCTCAG 6

RESULT 9
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LOCUS SALK_066400 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_066400, genomic survey sequence.
ACCESSION BH814452
VERSION BH814452.1 GI:20394043
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

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 Location/Qualifiers
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 /strain="Columbia 0"
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 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 10 a 1 c 14 g 5 t

BASE COUNT

ORIGIN
 Query Match 10.1%; Score 14; DB 28; Length 30;
 Best Local Similarity 77.3%; Pred. No. 3.5e+06;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 66 GTGCTGGAAGTTGGTTAGGAG 87
 |||||
Db 2 GTAGTGTAGAGGATTAGGAG 23

RESULT 10
BZ660808/c 26 bp DNA linear GSS 31-JAN-2003
LOCUS SALK_024268.26.95.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_024268.26.95.x, genomic survey sequence.

ACCESSION BZ660808
VERSION BZ660808.1 GI:28173955
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g55110.

FEATURES

source
 Location/Qualifiers
 1. 26
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_024268.26.95.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 10 a 1 c 14 g 5 t

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT 9 a 5 c 8 g 4 t
 ORIGIN
 Query Match 9.9%; Score 13.8; DB 29; Length 26;
 Best Local Similarity 88.2%; Pred. No. 3.8e+06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 55 TCTCTCCAGCGTG 71
 |||||
 Db 22 TCTCTCCAGCGTG 6
 |||||

RESULT 11
 AZ818209 27 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0088A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0088A08 F, genomic survey sequence.

ACCESSION AZ818209
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 27)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0088 row: A column: 08
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES

source
 1. .27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC2M0088A08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 2 g 12 t
 ORIGIN

Query Match 9.9%; Score 13.8; DB 28; Length 27;
 Best Local Similarity 72.0%; Pred. No. 3.8e+06;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 95 ATGGAGATTGGCTCCCAACTCTCTCC 119
 |||||
 Db 2 ATAAATAATGGTTCTCTACTCTCTCC 26
 |||||

RESULT 12

AZ990764

LOCUS

DEFINITION 2M0274F09R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0274F09 R, genomic survey sequence.

ACCESSION AZ990764
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 28)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0274 row: F column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES

source

1. .28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC2M0274F09"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

Mon Aug 25 09:45:55 2003

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

BASE COUNT 7 a 3 c 9 g 9 t
 ORIGIN
 Query Match 9.9%; Score 13.8; DB 28; Length 28;
 Best Local Similarity 72.0%; Pred. No. 3.9e+06;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 72 GAAGTTGGGTTAGGAGTACGGAGAT 96
 |||||
 Db 4 GAAGTTGGGCTTGTGAACGTACAT 28

RESULT 13
 AZ317165/c 24 bp DNA linear GSS 29-SEP-2000
 LOCUS
 DEFINITION
 Clone UGCM0035H03 R, genomic survey sequence.

ACCESSION
 AZ317165
 VERSION
 AZ317165.1 GI:10365702
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddu@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: H column: 03
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0035H03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0035H03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 8 c 1 g 8 t
 ORIGIN
 Query Match 9.8%; Score 13.6; DB 28; Length 24;
 Best Local Similarity 80.0%; Pred. No. 4.2e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 76 TTGGGTTAGGAGTACGGAGA 95
 |||||
 Db 24 TTGGGTTAGGAGTACGTAGA 5

RESULT 14
 AA868839 25 bp mRNA linear EST 04-JAN-1999
 LOCUS
 DEFINITION
 3' similar to TR:Q14679 Q14679 KIAA0173 PROTEIN. ; mRNA sequence.

ACCESSION
 AA868839
 VERSION
 AA868839.1 GI:2964284
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 25)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@xmail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LEML at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 1057 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1409814"
 /sex="male"
 /lab_host="DH10B"
 /clone_lib="Soares testis NHT"
 /note="Vector: pT730-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from clontech Laboratories
 , Inc., and primed with a Not I - oligo(dT) primer [5',
 TGTTACATCTGAAGTGGAGCGCCCAATTTTTCCTTTT 3'.
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia) digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 5 a 8 c 6 g 6 t

BASE COUNT
 ORIGIN

```

Query Match          9.8%;   Score 13.6;   DB 28;   Length 27;
Best Local Similarity 80.0%;   Pred. No. 4.4e+06;
Matches 16;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;
QY      28  ACCAGGCTCACAGCTGGAC 47

```

RESULT 16
AI635476/c
LOCUS
DEFINITION
AI635476 28 bp mRNA linear EST 26-APR-1999
t665803.x1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:2233468 3,
similar to TR_062107 Q62107 PROLINE-RICH SALIVARY PROTEIN ; contains
MER22.b1 M8RI repetitive element ;, mRNA sequence.
AI635476
AI635476.1 GI:4686806
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@cmail.nih.gov
Miscellaneous: Christopher Motaluk, M.D., Ph.D. Michael R.
Bancroft

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 cDNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
www-bio.llnl.gov/bbrp/image/image.html

```

FEATURES
  Location/Qualifiers
    1. .28
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2233468"
      /tissue_type="renal cell tumor"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP_Kid8"
      /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI;
      Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
      Average insert size 1.2 kb. Life Technologies catalog #:
      11524-014"
      6 a      8 g      0 t
      BASE COUNT
      ORIGIN
        Query Match          9.8%; Score 13.6; DB 9; Length 28;
        Best Local Similarity 67.98; Pred. No. 4.4e+06;
        Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
        Qy      58  CCTCCAGCGTGGTGGAAAGTTGGGTAGG 85
                |||||
        Db       28  CCCCCCGGGGGTGGTGGTTCGCTTGGG 1
                |||||

RESULT 17
BH810072/c
LOCUS
DEFINITION
  BH810072 28 bp DNA linear GSS 02-MAY-2005
  SALX 040645 Arabidopsis thaliana TDNA insertion lines Arabidopsis
  thaliana genomic clone SALX_040645, genomic survey sequence.
  BH810072
  ACCESSION

```

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g32895.
 Class: TDNA tagged.

FEATURES
 source
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_040694"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 7 a 9 c 4 g 8 t
 ORIGIN

Query Match 9.8%; Score 13.6; DB 28; Length 28;
 Best Local Similarity 80.0%; Pred. No. 4.4e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGGCAAGC 27
 |||||
 Db 27 GCTTGTAGCTGAGGAAAGC 8

RESULT 19
 BH810140/c
 LOCUS
 DEFINITION
 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_041353, genomic survey sequence.

ACCESSION
 VERSION
 BH810140.1 GI:20387958
 GSS.
 SOURCE
 Arabidopsis thaliana (thale cress)
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
 AUTHORS
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g32895.
 Class: TDNA tagged.

TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_041353"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
 AUTHORS
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g32895.
 Class: TDNA tagged.

FEATURES
 source
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_040645"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 7 a 9 c 4 g 8 t
 ORIGIN

Query Match 9.8%; Score 13.6; DB 28; Length 28;
 Best Local Similarity 80.0%; Pred. No. 4.4e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGGCAAGC 27
 |||||
 Db 27 GCTTGTAGCTGAGGAAAGC 8

RESULT 18
 BH810091/c
 LOCUS
 DEFINITION
 SALK_040694 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_040694, genomic survey sequence.

ACCESSION
 VERSION
 BH810091.1 GI:20387908
 GSS.
 SOURCE
 Arabidopsis thaliana (thale cress)
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
 AUTHORS
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies

TITLE
 JOURNAL
 COMMENT

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tcna_protocols.html

```

BASE COUNT      7 a      9 c      4 g      8 t
ORIGIN
Query Match      9.8%; Score 13.6; DB 28; Length 28;
Best Local Similarity 80.0%; Pred. No. 4.e+06;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGGACGAC 27
    |||||
Db 27 GCTTGTAGCTGAGGAAAGC 8

```

```

RESULT 20
AZ481978      27 bp      DNA      linear      GSS 04-OCT-2000
LOCUS      1M0306K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0306K11 R, genomic survey sequence.
ACCESSION      AZ481978.1 GI:10643043
VERSION
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: K column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306K11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```

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FEATURES
source
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306K11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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BASE COUNT      3 a      13 c      5 g      6 t
ORIGIN
Query Match      9.6%; Score 13.4; DB 28; Length 27;
Best Local Similarity 73.9%; Pred. No. 5.e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 105 GCTCCCACTCTCTCTATCTTA 127
    |||||
Db 5 GGTCCCCACTCTCTGTACCCCA 27

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RESULT 21
BE389833/c
LOCUS      601284336F1 NTH_MGC_44 Homo sapiens cDNA clone IMAGE:3606177 5',
DEFINITION      mRNA sequence.
ACCESSION      BE389833
VERSION
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
1 (bases 1 to 30)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cyabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM255 row: 9 column: 10
High quality sequence start: 10
High quality sequence stop: 28.
Location/Qualifiers
1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC 44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

FEATURES
source
1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC 44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

BASE COUNT      7 a      4 c      12 g      7 t
ORIGIN
Query Match      9.6%; Score 13.4; DB 10; Length 30;
Best Local Similarity 73.9%; Pred. No. 5.2e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 108 CCCAATCTCTCTCTATCTTAAG 130
    |||||
Db 26 CCAGCCTCGTACTTACGCTAAAG 4

```

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RESULT 22
AZ474193
LOCUS
DEFINITION
  AZ474193 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0290J02 R, genomic survey sequence.
ACCESSION
  AZ474193
VERSION
  AZ474193.1 GI:10632318
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0290 row: J column: 02
  Seq primer: CACACGAGAACACGTATGACC
  Class: plasmid ends
  High quality sequence stop: 30.
FEATURES
  source
  1..30
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clones="UUGC1M0290J02"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
  8 a 8 c 10 g 4 t
  BASE COUNT
  8 a 8 c 10 g 4 t
  ORIGIN
  Query Match 9.6%; Score 13.4; DB 28; Length 30;
  Best Local Similarity 73.9%; Pred. No. 5.2e+06;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

  Qy 26 GCACCGAGCTACACGTGGACC 48
  Db 8 GCACGAGACACACACGTGGACC 30
  COMMENT
  26 GCACCGAGCTACACGTGGACC 48
  8 GCACGAGACACACACGTGGACC 30
  4

RESULT 23
AB082245
LOCUS
DEFINITION
  AB082245 Drosophila melanogaster DNA, clone:1(2)SH2 0721, genomic survey
  sequence.
ACCESSION
  AB082245
VERSION
  AB082245.1 GI:23307282
KEYWORDS
  GSS.
SOURCE
  Drosophila melanogaster (fruit fly)
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
  1
REFERENCE
  Oh, S.W., Kingsley, T., Shin, H.H., Zheng, Z., Chen, H.W., Chen, X.,
  Wang, H., Ruan, P., Moody, M. and Hou, S.X.
  A p-element insertion screen identified mutations in 455 novel
  essential genes in Drosophila
  Genetics 163 (1), 195-201 (2003)
  22474228
  12586707
REFERENCE
  2 (bases 1 to 30)
  Direct Submission
  Authors
  Oh, S., Kingsley, T., Shin, H., Zheng, Z., Chen, H. and Hou, S.
  Submitted (24-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,
  National Institutes of Health, National Cancer Institute,
  Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA
  (E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,
  Fax:1-301-846-6145)
FEATURES
  source
  1..30
  /organism="Drosophila melanogaster"
  /mol_type="genomic DNA"
  /db_xref="taxon:7227"
  /clone="1(2)SH2 0721"
  7 a 6 c 12 g 5 t
  BASE COUNT
  7 a 6 c 12 g 5 t
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  Query Match 9.6%; Score 13.4; DB 29; Length 30;
  Best Local Similarity 73.9%; Pred. No. 5.2e+06;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

  Qy 6 GGCCTGTAGCAGACAGCGACGA 28
  Db 4 GGCCTGTAGCAGACAGCGGTCA 26

RESULT 24
TAI79D12P/c
LOCUS
DEFINITION
  TAI79D12P T. brucei sheared genomic DNA clone 179d12, forward sequence,
  genomic survey sequence.
ACCESSION
  AL474655
VERSION
  AL474655.1 GI:11839841
KEYWORDS
  GSS.
SOURCE
  Trypanosoma brucei
  Trypanosoma brucei
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
  1 (bases 1 to 30)
REFERENCE
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
  Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
  Melville, S.B., Rajandream, M.A. and Barrell, B.G.
  Direct Submission
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
  nh@sanger.ac.uk
  Constructed at the Institute for Genomic Research (TIGR),
  Rockville, MD. Genomic DNA isolated from a cloned population of
  Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
  to give a tight size distribution (

```

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: neleaved@igr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
Location/Qualifiers
1..30
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="179d12"

BASE COUNT 10 a 7 c 6 g 7 t

ORIGIN

Query Match 9.6%; Score 13.4; DB 29; Length 30;
Best Local Similarity 73.9%; Pred. No. 5.2e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 60 TCCAGCGTGGTGGAGTTGGGTT 82
||||| ||||| ||||| |||||
DB 30 TCCACCGTCGTAGAAATGTGTT 8

RESULT 25

AZ421118/c
LOCUS AZ421118 21 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0199D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0199D16 F, genomic survey sequence.
ACCESSION AZ421118
VERSION AZ421118.1 GI:10545131
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: D column: 16
Seq primer: CCGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0199D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 8 c 7 g 4 t

ORIGIN

Query Match 9.5%; Score 13.2; DB 28; Length 21;
Best Local Similarity 83.3%; Pred. No. 5.2e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 31 AGGCTCACAGCTGGAAACC 48
||||| ||||| ||||| |||||
DB 21 AGGCTCACAGCTGGTCCC 4

Search completed: August 22, 2003, 11:04:43

Job time : 1699 secs